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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:29:22 ; Search time 23.54 Seconds
(without alignments)
321.662 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 1633
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	415	25.4	299	4	US-09-188-930-331	Sequence 331, App
2	415	25.4	299	4	US-09-462-270-2	Sequence 2, Appli
3	403	24.7	299	4	US-09-188-930-189	Sequence 189, App
4	283	17.3	205	4	US-09-462-270-4	Sequence 4, Appli
5	242.5	14.8	319	1	US-08-597-495B-22	Sequence 22, Appl
6	242.5	14.8	319	4	US-09-068-051A-22	Sequence 22, Appl
7	240.5	14.7	318	4	US-09-068-051A-32	Sequence 32, Appl
8	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
9	173.5	10.6	365	4	US-08-928-383B-2	Sequence 2, Appli
10	172.5	10.6	365	2	US-08-979-424-3	Sequence 3, Appli
11	172.5	10.6	365	4	US-09-272-496-2	Sequence 2, Appli
12	171.5	10.5	390	2	US-08-979-424-1	Sequence 1, Appli
13	166	10.2	1101	3	US-08-986-485-2	Sequence 2, Appli
14	160	9.8	869	1	US-08-374-834-16	Sequence 16, Appl
15	160	9.8	869	2	US-08-644-271-29	Sequence 29, Appl
16	156.5	9.6	365	4	US-08-928-383B-23	Sequence 23, Appl
17	156.5	9.6	365	4	US-08-928-383B-24	Sequence 24, Appl
18	151.5	9.3	365	4	US-08-928-383B-26	Sequence 26, Appl
19	151	9.2	1091	3	US-08-986-485-5	Sequence 5, Appli
20	150	9.2	1297	4	US-09-540-245A-17	Sequence 17, Appl
21	148	9.1	607	2	US-08-752-307B-12	Sequence 12, Appl
22	147.5	9.0	501	2	US-08-408-095-31	Sequence 31, Appl
23	147	9.0	95	4	US-08-928-383B-18	Sequence 18, Appl
24	147	9.0	1395	4	US-09-540-245A-15	Sequence 15, Appl
25	146.5	9.0	478	5	PCT-US95-08493-15	Sequence 15, Appl
26	146.5	9.0	860	5	PCT-US95-08493-19	Sequence 19, Appl
27	146.5	9.0	868	5	PCT-US95-08493-21	Sequence 21, Appl
28	144.5	8.8	698	2	US-08-602-725-36	Sequence 36, Appl
29	144.5	8.8	734	2	US-08-389-459A-17	Sequence 17, Appl
30	144.5	8.8	734	3	US-08-987-867A-17	Sequence 17, Appl
31	144.5	8.8	868	1	US-08-374-834-1	Sequence 1, Appli
32	144.5	8.8	868	2	US-08-644-271-1	Sequence 1, Appli
33	144	8.8	1651	4	US-09-540-245A-18	Sequence 18, Appl
34	142.5	8.7	1260	4	US-08-506-296B-21	Sequence 21, Appl
35	141	8.6	338	2	US-08-414-657D-60	Sequence 60, Appl
36	141	8.6	642	1	US-08-217-299-1	Sequence 1, Appli
37	141	8.6	1501	2	US-08-447-464-3	Sequence 3, Appli
38	141	8.6	1501	2	US-08-716-679-3	Sequence 3, Appli
39	139.5	8.5	612	2	US-08-752-307B-11	Sequence 11, Appl
40	139.5	8.5	983	4	US-09-412-554A-2	Sequence 2, Appli
41	139.5	8.5	1268	4	US-08-506-296B-28	Sequence 28, Appl
42	139.5	8.5	1447	4	US-09-041-886-25	Sequence 25, Appl
43	139.5	8.5	1447	5	PCT-US94-05277-2	Sequence 2, Appli
44	139	8.5	310	2	US-08-414-657D-45	Sequence 45, Appl
45	139	8.5	338	2	US-08-414-657D-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 8.8e-34;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

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Qy      18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
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Db      15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy      78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
           | ::|||      |   |  | :   :||| |:  | | :|:        |: ::||| |
Db      73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy     138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
           |  |   ||::  :|  | | | | :| |   |:|::: : :||: ::   | |||: :
Db     131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy     198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
           |  || |||: :   |:|:| | | |  |          ||  : |:  |:  ||| ||:|
Db     191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy     257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
           ::  ||  || || |  :|:   | |       | | : |   ||:|:  |||::
Db     251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299
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RESULT 2

US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match 25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 8.8e-34;
Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;

Qy 18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
Db 15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy 78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
Db 73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy 138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
Db 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy 198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
Db 191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILL 250

Qy 257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
Db 251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEGEFKQTSSFLV 299

RESULT 3
US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)
US-09-188-930-189

Query Match 24.7%; Score 403; DB 4; Length 299;
Best Local Similarity 33.1%; Pred. No. 1.4e-32;
Matches 98; Conservative 50; Mismatches 134; Indels 14; Gaps 6;

Qy 18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
Db 15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy 78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
Db 73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy 138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
Db 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy 198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ-DMEVYDLNIAGIIGGVLVVLIVL 256
Db 191 NPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTXILL 250

Qy 257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
Db 251 GILVFGIWFAYSRGHFDRTKKGTSSKK-------VIYSQPSARSEXEFKQTSSFLV 299

RESULT 4
US-09-462-270-4
; Sequence 4, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 205
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-4

Query Match 17.3%; Score 283; DB 4; Length 205;
Best Local Similarity 33.5%; Pred. No. 9.8e-21;
Matches 64; Conservative 34; Mismatches 89; Indels 4; Gaps 3;

Qy 18 FFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
Db 15 FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72

Qy 78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQV 137
Db 73 VCYNNKITASYEDRV-TFLPTGITFKSVTREDTGTYTC-MVSEEGGNSYGEVKVKLIVLV 130

Qy 138 KPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
Db 131 PPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVL 190

Qy 198 NSETGTLVFNA 208
Db 191 NPTTGELVFES 201

RESULT 5
US-08-597-495B-22
; Sequence 22, Application US/08597495B

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; Patent No. 5712369
; GENERAL INFORMATION:
;   APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
;   APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;   APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;   APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;   TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
;   TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Felfe & Lynch
;     STREET: 805 Third Avenue
;     CITY: New York City
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10022
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: PC-DOS
;     SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/597,495B
;     FILING DATE: 02-Feb-1996
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/511,876
;     FILING DATE: 04-Aug-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hanson, No. 5712369man D.
;     REGISTRATION NUMBER: 30,946
;     REFERENCE/DOCKET NUMBER: LUD 5316.1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 688-9200
;     TELEFAX: (212) 838-3884
;  INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 319 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
US-08-597-495B-22


  Query Match             14.8%;  Score 242.5;  DB 1;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 2.2e-16;
  Matches   80;  Conservative   49;  Mismatches  123;  Indels   59;  Gaps   12;

Qy      29 IEAVNLKSSNRNPVVHEFESVELSCIITHSQTS--DPRIEWKKIQDGQTTYVY---FDNK 83
           ::|:::::        : :|| | |   |: ||  :  |:| |:    |  |    | ||
Db      19 VDAISVETPQDVLRASQGKSVTLPCTY-HTSTSSREGLIQWDKLLLTHTERVVIWPFSNK 77

Qy      84 --IQGDL----------AGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITI 131
             | |:|          | ::|     |: |  :| :|:  | | |  ::| :   :  :
Db      78 NYIHGELYKNRVSISNNAEQSD----ASITIDQLTMADNGTYECSVSLMSDLEGNTKSRV 133

Qy     132 ELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDV-----PLPTDSRA 186
            |:| | |  | | |     :|    | ||  || | | |||  | ::     ||   :
Db     134 RLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASG 193

Qy     187 NPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAG--------AARCEGQDMEVY 238
           |               :    :  | || | | :||: |         | |    :: :|
Db     194 QP--------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALY 238

Qy     239 DLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDG----ESYKSPGKHDGVNYI 294
                ||  ||:  ||:: :| :  ||   :      |:|     |:|: | :
Db     239 ----VGIAVGVVAALIIIGII-IYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR 293

Qy     295 RTSEEGDFRHK 305
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Db     294 EREEEDDYRQE 304


RESULT   6
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US-09-068-051A-22
; Sequence 22, Application US/09068051A
; Patent No. 6291235
;   GENERAL INFORMATION:
;       APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
;                  Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;                  Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;                  Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;       TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
;                           Associated Nucleic Acid Molecules, Protein And Peptides
;       NUMBER OF SEQUENCES: 33
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski LLP
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: Wordperfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/068,051A
;            FILING DATE: 10-Dec-1998
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/597,495
;            FILING DATE: 02-Feb-1996
;            APPLICATION NUMBER: 08/511,876
;            FILING DATE: 04-Aug-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hanson, No. 6291235man D.
;            REGISTRATION NUMBER: 30,946
;            REFERENCE/DOCKET NUMBER: LUD 5316.2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 318-3168
;            TELEFAX: (212) 752-5958
;  INFORMATION FOR SEQ ID NO: 22
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 319 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-068-051A-22


  Query Match             14.8%;  Score 242.5;  DB 4;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 2.2e-16;
  Matches   80;  Conservative   49;  Mismatches  123;  Indels   59;  Gaps   12;

Qy      29 IEAVNLKSSNRNPVVHEFESVELSCIITHSQTS--DPRIEWKKIQDGQTTYVY---FDNK 83
           ::|:::::        : :|| | |   |: ||  :  |:| |:    |  |    | ||
Db      19 VDAISVETPQDVLRASQGKSVTLPCTY-HTSTSSREGLIQWDKLLLTHTERVVIWPFSNK 77

Qy      84 --IQGDL----------AGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITI 131
             | |:|          | ::|     |: |  :| :|:  | | |  ::| :   :  :
Db      78 NYIHGELYKNRVSISNNAEQSD----ASITIDQLTMADNGTYECSVSLMSDLEGNTKSRV 133

Qy     132 ELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDV-----PLPTDSRA 186
            |:| | |  | | |     :|    | ||  || | | |||  | ::     ||   :
Db     134 RLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASG 193

Qy     187 NPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAG--------AARCEGQDMEVY 238
           |               :    :  | || | | :||: |         | |    :: :|
Db     194 QP--------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALY 238

Qy     239 DLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDG----ESYKSPGKHDGVNYI 294
                ||  ||:  ||:: :| :  ||   :      |:|     |:|: | :
Db     239 ----VGIAVGVVAALIIIGII-IYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR 293

Qy     295 RTSEEGDFRHK 305
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Db    294 EREEEDDYRQE 304


RESULT   7
US-09-068-051A-32
; Sequence 32, Application US/09068051A
; Patent No. 6291235
;   GENERAL INFORMATION:
;        APPLICANT: Old, Lloyd J.;  Welt, Sydney; Ritter, Gerd;
;                   Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;                   Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;                   Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;        TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
;                            Associated Nucleic Acid Molecules, Protein And Peptides
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Wordperfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/068,051A
;             FILING DATE: 10-Dec-1998
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/597,495
;             FILING DATE: 02-Feb-1996
;             APPLICATION NUMBER: 08/511,876
;             FILING DATE: 04-Aug-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6291235man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5316.2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 32
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 318 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-068-051A-32


  Query Match             14.7%;  Score 240.5;  DB 4;  Length 318;
  Best Local Similarity   24.9%;  Pred. No. 3.6e-16;
  Matches   73;  Conservative   37;  Mismatches  122;  Indels   61;  Gaps   10;

Qy      48 SVELSCII-THSQTSDPRIEWKKIQDGQT-----------TYVY---FDNKIQGDLAGRT 92
           || | |   |:    :  |:| |:   ||            |:|   ::|:::
Db      37 SVTLPCTYNTYVSDREGFIQWDKLLRSQTERVVTWNFVTKKYIYGNRYENRVR---VSND 93

Qy      93 DVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPV 152
              |: |  :|  |:  | | |  ::|:    :  : |:| | |  | | |   : :
Db      94 AELSNASITIDQLTMDDNGTYECSVSLMSDQDVNAKSRVRLLVLVPPSKPDCSIQGEMVI 153

Qy     153 GKTATLQCQESEGYPRPHYSW-----YRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
           |    | |  :|| | | |||          ||       |               |:
Db     154 GNNIQLTCHSAEGSPSPQYSWKSYNAQNQQRPLTQPVSGEP--------------LLLK 198

Qy     208 AVHKDDSGQYYCIASNDAGAARCE--------GQDMEVYDLNIAGIIGGVLVVLIVLAVI 259
            :  : :| | | :||| |   |           :: :|    ||| | | | ||:: ||
Db     199 NISTETAGYYICTSSNDVGIESCNITVAPRPPSMNIALY----AGIAGSVFVALIIIGVI 254

Qy     260 TMGICCAYRRGCFISSKQDGE-------SYKSPGKHDGVNYIRTSEEGDFRHK 305
              ||  :       || |       :|: | |          :| | ||:
Db     255 VYCCCCREKD----DKDQDREDARPNRAAYQVPKKEQKEISRGREDEDDHRHE 303


RESULT   8
US-09-175-928-2
; Sequence 2, Application US/09175928A
; Patent No. 6312921
; GENERAL INFORMATION:
;  APPLICANT: Jacobs, Kenneth
;  APPLICANT: McCoy, John M.
;  APPLICANT: LaVallie, Edward R.
;  APPLICANT: Collins-Racie, Lisa A.
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maurice
;  APPLICANT: Mi, Sha
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: 6006B.AJ172A
;  CURRENT APPLICATION NUMBER: US/09/175,928A
;  CURRENT FILING DATE: 1998-10-20
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-175-928-2


  Query Match             12.1%;  Score 197.5;  DB 4;  Length 387;
  Best Local Similarity   26.4%;  Pred. No. 1e-11;
  Matches   76;  Conservative   41;  Mismatches  118;  Indels   53;  Gaps   12;

Qy      18 FFLLLLFRGCM-----IEAVNLKSSNRNPVVHEFESVELSCIITHSQTSDPR--IEW--- 67
           |: : |   |:      :  | :      |  |    :| | || | :  |  :  |:|
Db       5 FWKVFLILSCLAGQVSVVQVTIPDGFVNVTVG--SNVTLICIYTTTVASREQLSIQWSFF 62

Qy      68 -KK---------IQDGQTTYV-YFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE 116
            ||          | ||    :  | ::| |     ::  |  |: | ::  :|| || |:
Db      63 HKKEMEPISIYFSQGGQAVAIGQFKDRITG-----SNDPGNASITISHMQPADSGIYICD 117

Qy     117 VVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYR- 175
           |    |    ::  : : | ||+|  |:| :       | | :| |  : | | | | |::
Db     118 VNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLSCLSALGTPSPVYYWHKL 177

Qy     176 --NDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQ 233
              |: :|     ||            || ||   :   : | | | | |  | : ||
Db     178 EGRDI-VPVKENFNP----------TTGILVIGNLTNFEQGYYQCTAINRLGNSSCE-- 223

Qy     234 DMEVYDLNIA----GIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQ 277
           ||  :    ||| | |:  :| | | : : |  |       :|:
Db     224 ----IDLTSSHPEVGIIVGALIGSLVGAAIIISVVCFARNKAKAKAKE 267


RESULT   9
US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
;  GENERAL INFORMATION:
;    APPLICANT:  Robert W. Finberg, Jeffrey M. Bergelson,
;    APPLICANT:  and Marshall S. Horwitz
;    TITLE OF INVENTION:  CAR, A No. 6210921el Coxsackievirus and Adenovirus
;    TITLE OF INVENTION:  Receptor
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
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;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/928,383B
;       FILING DATE:  12-SEP-1997
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/026,100
;       FILING DATE:  13-SEP-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mandragouras, Amy E.
;       REGISTRATION NUMBER:  36,207
;       REFERENCE/DOCKET NUMBER:  DFN-020
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  365 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-928-383B-2


  Query Match             10.6%;  Score 173.5;  DB 4;  Length 365;
  Best Local Similarity   26.4%;  Pred. No. 2.4e-09;
  Matches   70;  Conservative   37;  Mismatches  113;  Indels   45;  Gaps   12;

Qy      47 ESVELSCIITHS-QTSDP-RIEW-------KKIQDGQTTYVYFDNKIQG----DLAGRTD 93
           |:  | |  | | :   |  |||       :|:   |   :|  :||      || ||
Db      35 ETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVD--QVIILYSGDKIYDDYYPDLKGRVH 92

Qy      94 V------FGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP 147
                 |  |: : |:  ||   |:|:|        |    | |:| |||    | :
Db      93 FTSNDLKSGDASINVTNLQLSDIGTYQCKV---KKAPGVANKKIHLVVLVKPSGARCYVD 149

Qy     148 AAVPVGKTATLQCQESEGYPRPHYSWYR--NDVPLPTDSRANPRFQNSSFHVNSETGTLV 205
             :  :|    ::|:  ||     | | :  :  :|| | |     :|   | : :
Db     150 GSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPTSSLA--EMTSSVISVKNAS---- 203

Qy     206 FNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLV-VLIVLAVITMGIC 264
               : || | |   |  |: :|  :   |   | ||:| | ::  |: ||:| : |
Db     204 -----SEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLLALALIGLIIF 258

Qy     265 CAYRRGCFISSKQDGESYKSPGKHD 289
           |  :       |:  | |:    ||
Db     259 CCRK-------KRREEKYEKEVHHD 276


RESULT  10
US-08-979-424-3
; Sequence 3, Application US/08979424
; Patent No. 5942606
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VIRAL RECEPTOR PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  365 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1946351
US-08-979-424-3


  Query Match             10.6%;  Score 172.5;  DB 2;  Length 365;
  Best Local Similarity   25.9%;  Pred. No. 3.1e-09;
  Matches   68;  Conservative   38;  Mismatches  116;  Indels   41;  Gaps   11;

Qy      47 ESVELSCIITHS-QTSDP-RIEW-------KKIQDGQTTYVYFDNKIQG----DLAGRTD 93
           |:  | |  | | :   |  |||       :|:   |   :|  :||      || ||
Db      35 ETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVD--QVIILYSGDKIYDDYYPDLKGRVH 92

Qy      94 V------FGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP 147
                 |  |: : |:  ||   |:|:|        |    | |:| |||    | :
Db      93 FTSNDLKSGDASINVTNLQLSDIGTYQCKV---KKAPGVANKKIHLVVLVKPSGARCYVD 149

Qy     148 AAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
             :  :|    ::|:  ||     | | :      :||:  |    :|:     :  :
Db     150 GSEEIGSDFKIKCEPKEGSLPLQYEWQK-----LSDSQKMP----TSWLAEMTSSVISVK 200

Qy     208 AVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLV-VLIVLAVITMGICCA 266
               : || | |   |  |: :|  :   |   | ||:| | ::  |: ||:| : | |
Db     201 NASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCC 260

Qy     267 YRRGCFISSKQDGESYKSPGKHD 289
             :       |:  | |:    ||
Db     261 RK-------KRREEKYEKEVHHD 276


RESULT  11
US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
;  APPLICANT: DeGregori, James
;  TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
;  FILE REFERENCE: 90-98
;  CURRENT APPLICATION NUMBER: US/09/272,496
;  CURRENT FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: US 60/092782
;  EARLIER FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-272-496-2
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  Query Match           10.6%;  Score 172.5;  DB 4;  Length 365;
  Best Local Similarity  25.9%;  Pred. No. 3.1e-09;
  Matches   68;  Conservative   38;  Mismatches  116;  Indels   41;  Gaps   11;

Qy      47 ESVELSCIITHS-QTSDP-RIEW-------KKIQDGQTTYVYFDNKIQG----DLAGRTD 93
           |:  | |  | | :   |  |||        :|:   |   :|  :||      || ||
Db      35 ETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVD--QVIILYSGDKIYDDYYPDLKGRVH 92

Qy      94 V------FGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP 147
                 |  |: : |:  ||   |:|:|        |    | |:| |||    | :
Db      93 FTSNDLKSGDASINVTNLQLSDIGTYQCKV---KKAPGVANKKIHLVVLVKPSGARCYVD 149

Qy     148 AAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
           :  :|    ::|:  ||     | | :      :||:  |    :|:     :  :
Db     150 GSEEIGSDFKIKCEPKEGSLPLQYEWQK-----LSDSQKMP----TSWLAEMTSSVISVK 200

Qy     208 AVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLV-VLIVLAVITMGICCA 266
                : || | |   |  |: :|  :   |   | ||:| | ::  |: ||:| : | |
       201 NASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCC 260

Qy     267 YRRGCFISSKQDGESYKSPGKHD 289
           :       |:  | |:    ||
Db     261 RK-------KRREEKYEKEVHHD 276


RESULT  12
US-08-979-424-1
; Sequence 1, Application US/08979424
; Patent No. 5942606
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VIRAL RECEPTOR PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  390 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGFET03
;      CLONE:  1232054
US-08-979-424-1
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  Query Match           10.5%;  Score 171.5;  DB 2;  Length 390;
  Best Local Similarity  24.9%;  Pred. No. 4.3e-09;
  Matches   80;  Conservative   36;  Mismatches  122;  Indels   83;  Gaps   15;

Qy       2 ALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQTS 61
           ||:   | :|  ||                    :||   |   | | :   | : |
Db      22 ALAPPSRAQLQLHLP------------------ANRLQAVEGGEVVLPAWYTLHGEVS 61

Qy      62 D------PRIEW----KKIQDGQTTYVYFDNKIQGDLAGRTDVFG----KTSLRIWNVTR 107
                 | : |    |: :|   :|:   | :     | : |:       |||:  :
Db      62 SSQPWEVPFVMWFFKQKEKEDQVLSYI---NGVTTSKPGVSLVYSMPSRNLSLRLEGLQE 118

Qy     108 SDSAIYRCEVVALNDRKEVDE----ITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQES 163
            ||  | |  | : |::          |:|| | | |  | ||:     ||   || ||
Db     119 KDSGPYSCS-VNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSP 177

Qy     164 EGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFH---VNSETGTLVFNAVHKDDSGQYYCI 220
               |  | |           |  | ||  :|    ::   |:|    :    :| | |
Db     178 RSKPAVQYQW----------DRQLPSFQ--TFFAPALDVIRGSLSLTNLSSSMAGVYVCK 225

Qy     221 ASNDAGAARCE-------GQDMEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFI 273
           | |: | |:|         |    |    :|| : | || | :||    |:   | |
Db     226 AHNEVGTAQCNVTLEVSTGPGAAV----VAGAVVGTLVGLGLLA----GLVLLYHR---- 273

Qy     274 SSKQDGESYKSPG---KHDGV 291
                 |:: : |     | | :
Db     274 ----RGKALEEPANDIKEDAI 290


RESULT  13
US-08-986-485-2
; Sequence 2, Application US/08986485
; Patent No. 6046030
;  GENERAL INFORMATION:
;    APPLICANT:  WU, SHUJIAN
;    APPLICANT:  SWEET, RAYMOND
;    APPLICANT:  TRUNEH, ALEMSEGED
;    TITLE OF INVENTION:  A HUMAN LIG-1 HOMOLOG (HLIG-1)
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/986,485
;      FILING DATE:  08-DEC-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/059,448
;      FILING DATE:  22-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1101 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-986-485-2


  Query Match             10.2%;  Score 166;  DB 3;  Length 1101;
  Best Local Similarity   22.8%;  Pred. No. 7e-08;
  Matches   66;  Conservative   44;  Mismatches  101;  Indels   78;  Gaps   16;

Qy      51 LSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGR---------TDVFGKTSLR 101
           | |  |     :|:| |:|  || | :           | |          |||  | ::
Db     626 LECAATGH--PNPQIAWQK--DGGTDFP----------AARERRMHVMPDDDVFFITDVK 671

Qy     102 IWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIP---AAVPVGKTATL 158
           |      |: :| |   | |    :       :::    ||   :|     | ||:|  |
Db     672 I-----DDAGVYSC--TAQNSAGSISANATLTVLE----TPSLVVPLEDRVVSVGETVAL 720

Qy     159 QCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYY 218
           || :: | | |  :|:: | ||    |          |: :   ||   |  :|:|:|
Db     721 QC-KATGNPPPRITWFKGDRPLSLTER---------HHLTPDNQLLVVQNVVAEDAGRYT 770

Qy     219 CIASNDAGAARCEGQDMEVYDLNIAGIIG--------GVLVVLIVLAVI---TMGICCAY 267
           |  ||  |  |   |      |::    |        |:  : :| :::    : :|  |
Db     771 CEMSNTLGTERAHSQ------LSVLPAAGCRKDGTTVGIFTIAVVSSIVLTSLVWVCIIY 824

Qy     268 RRGCFISSKQDGESYKSPGKHDGV------NYIRTSEEGDFRHKSSFVI 310
           :      :::  | |      : |      :|:  | :|    :   |:
Db     825 Q------TRKKSEEYSVTNTDETVVPPDVPSYL--SSQGTLSDRQETVV 865


RESULT  14
US-08-374-834-16
; Sequence 16, Application US/08374834
; Patent No. 5656473
;  GENERAL INFORMATION:
;    APPLICANT:  Valenzuela, et al.
;    TITLE OF INVENTION:  NOVEL TYROSINE KINASE RECEPTOR
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,834
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/095,658
;      FILING DATE:  21-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cobert, Robert J.
;      REGISTRATION NUMBER:  36,108
;      REFERENCE/DOCKET NUMBER:  REG 190A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 345-7400
;      TELEFAX:  (914) 345-7721
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  869 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-374-834-16


  Query Match             9.8%;  Score 160;  DB 1;  Length 869;
  Best Local Similarity   28.8%;  Pred. No. 2e-07;
  Matches   70;  Conservative   23;  Mismatches   82;  Indels   68;  Gaps   11;

Qy      28 MIEAVNLKSSNRNPVVHEFESVELS---------CIITHSQTSD---------------- 62
           | | ||:      |:||    |  |          | |  :| |
Db       1 MRELVNI------PLVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVATFMCAVESY 54

Qy      63 --PRIEWKK----IQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE 116
             | | :    |:   | |   :|   | |           | | :|  ||  || |
Db      55 PQPEISWTRNKILIKLFDTRYSIREN---GQL----------LTILSVEDSDDGIYCC- 99

Qy     117 VVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPV--GKTATLQCQESEGYPRPHYSWY 174
           | |      |    | |::||   : | |  | :  |  | | |  : | |:|  ||
Db     100 -TANNGVGGAVESCGALQVKMKP--KITRPPINVKIIEGLKAVLPC-TTMGNPKPSVSWI 155

Qy     175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
           : | ||  :||             |:|:|  : | |:|:||| |:| |  | |  :
Db     156 KGDSPLRENSRI----------AVLESGSLRIHNVQKEDAGQYRCVAKNSLGTAYSKVVK 205

Qy     235 MEV 237
           :||
Db     206 LEV 208


RESULT  15
US-08-644-271-29
; Sequence 29, Application US/08644271
; Patent No. 5814478
;  GENERAL INFORMATION:
;    APPLICANT:  Valenzuela, et al.
;    TITLE OF INVENTION:  NOVEL TYROSINE KINASE RECEPTORS
;    TITLE OF INVENTION:  AND LIGANDS
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill Road
;      CITY:  Tarrytown
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/644,271
;      FILING DATE:  10-MAY-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 60/008,657
;      FILING DATE:  15-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cobert, Robert J
;      REGISTRATION NUMBER:  36,108
;      REFERENCE/DOCKET NUMBER:  REG 195A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  869 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-644-271-29


  Query Match             9.8%;  Score 160;  DB 2;  Length 869;
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  Best Local Similarity   28.8%;  Pred. No. 2e-07;
  Matches   70;  Conservative   23;  Mismatches   82;  Indels   68;  Gaps   11;

Qy      28 MIEAVNLKSSNRNPVVHEFESVELS---------CIITHSQTSD---------------- 62
           | | ||:      |:||    |  |          | |  :| |
Db       1 MRELVNI------PLVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVATFMCAVESY 54

Qy      63 --PRIEWKK----IQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE 116
             | | | :    |:   | |   :|   | |           | | :|  ||  || |
Db      55 PQPEISWTRNKILIKLFDTRYSIREN---GQL-----------LTILSVEDSDDGIYCC- 99

Qy     117 VVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPV--GKTATLQCQESEGYPRPHYSWY 174
             | |       |    | |::||   : | |  | :  |  | | |  : | |:|  ||
Db     100 -TANNGVGGAVESCGALQVKMKP--KITRPPINVKIIEGLKAVLPC-TTMGNPKPSVSWI 155

Qy     175 RNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
           : | ||  :||             |:|:|  : | |:|:||| |:| |  | | :
Db     156 KGDSPLRENSRI----------AVLESGSLRIHNVQKEDAGQYRCVAKNSLGTAYSKVVK 205

       235 MEV 237
           :||
       206 LEV 208


Search completed: September 19, 2002, 17:33:15
Job time: 233 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:33:15 ; Search time 23.54 Seconds
(without alignments)
321.662 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 1637
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

1 number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	424	25.9	299	4	US-09-188-930-331	Sequence 331, App
2	424	25.9	299	4	US-09-462-270-2	Sequence 2, Appli
3	412	25.2	299	4	US-09-188-930-189	Sequence 189, App
4	288	17.6	205	4	US-09-462-270-4	Sequence 4, Appli
5	228.5	14.0	319	1	US-08-597-495B-22	Sequence 22, Appl
6	228.5	14.0	319	4	US-09-068-051A-22	Sequence 22, Appl
7	215.5	13.2	318	4	US-09-068-051A-32	Sequence 32, Appl
8	197.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
9	169.5	10.4	390	2	US-08-979-424-1	Sequence 1, Appli
10	160.5	9.8	365	4	US-08-928-383B-2	Sequence 2, Appli
11	159.5	9.7	365	2	US-08-979-424-3	Sequence 3, Appli
12	159.5	9.7	365	4	US-09-272-496-2	Sequence 2, Appli
13	157.5	9.6	1101	3	US-08-986-485-2	Sequence 2, Appli
14	155.5	9.5	612	2	US-08-752-307B-11	Sequence 11, Appl
15	155.5	9.5	1268	4	US-08-506-296B-28	Sequence 28, Appl
16	154	9.4	1501	2	US-08-447-464-3	Sequence 3, Appli
17	154	9.4	1501	2	US-08-716-679-3	Sequence 3, Appli
18	153	9.3	1651	4	US-09-540-245A-18	Sequence 18, Appl
19	152.5	9.3	869	1	US-08-374-834-16	Sequence 16, Appl
20	152.5	9.3	869	2	US-08-644-271-29	Sequence 29, Appl
21	152	9.3	95	4	US-08-928-383B-18	Sequence 18, Appl
22	150.5	9.2	698	2	US-08-602-725-36	Sequence 36, Appl
23	150.5	9.2	734	2	US-08-389-459A-17	Sequence 17, Appl
24	150.5	9.2	734	3	US-08-987-867A-17	Sequence 17, Appl
25	147	9.0	365	4	US-08-928-383B-23	Sequence 23, Appl
26	147	9.0	365	4	US-08-928-383B-24	Sequence 24, Appl
27	146.5	8.9	315	2	US-08-414-657D-47	Sequence 47, Appl
28	146.5	8.9	338	2	US-08-414-657D-42	Sequence 42, Appl
29	146.5	8.9	338	2	US-08-414-657D-43	Sequence 43, Appl
30	146.5	8.9	1297	4	US-09-540-245A-17	Sequence 17, Appl
31	145.5	8.9	252	2	US-08-414-657D-57	Sequence 57, Appl
32	145.5	8.9	287	2	US-08-414-657D-49	Sequence 49, Appl
33	145.5	8.9	310	2	US-08-414-657D-45	Sequence 45, Appl
34	145.5	8.9	338	2	US-08-414-657D-60	Sequence 60, Appl
35	145.5	8.9	478	5	PCT-US95-08493-15	Sequence 15, Appl
36	145.5	8.9	860	5	PCT-US95-08493-19	Sequence 19, Appl
37	145.5	8.9	868	5	PCT-US95-08493-21	Sequence 21, Appl
38	144.5	8.8	252	2	US-08-414-657D-56	Sequence 56, Appl
39	144.5	8.8	287	2	US-08-414-657D-48	Sequence 48, Appl
40	144.5	8.8	304	2	US-08-414-657D-44	Sequence 44, Appl
41	144.5	8.8	308	2	US-08-414-657D-46	Sequence 46, Appl
42	144.5	8.8	325	2	US-08-414-657D-2	Sequence 2, Appli
43	144.5	8.8	325	2	US-08-414-657D-41	Sequence 41, Appl
44	144	8.8	501	2	US-08-408-095-31	Sequence 31, Appl
45	143.5	8.8	868	1	US-08-374-834-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match 25.9%; Score 424; DB 4; Length 299;
Best Local Similarity 32.8%; Pred. No. 2.5e-35;
Matches 101; Conservative 48; Mismatches 137; Indels 22; Gaps 7;

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Db       9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy      68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
             | | : |  | ::|||      |   |  | :   :||| |:  | | :|:
Db      63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy     128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
           |: ::| | | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db     121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy     188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
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Db     181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy     247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
             ||| | :| ::  ||  || ||:|  |:  |    | |             ||:|
Db     241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy     303 RHKSSFVI 310
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Db    292 KQTSSFLV 299


RESULT   2
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
;  APPLICANT:  SmithKline Beecham Corporation
;  TITLE OF INVENTION:  Human F11 Antigen: A Cell Surface
;  TITLE OF INVENTION:  Receptor   Involved in Platelet Aggregation
;  FILE REFERENCE:  GH-70150US
;  CURRENT APPLICATION NUMBER: US/09/462,270
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/052,186
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
    LENGTH: 299
    TYPE: PRT
,   ORGANISM: HOMO SAPIENS
US-09-462-270-2


  Query Match             25.9%;  Score 424;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 2.5e-35;
  Matches  101;  Conservative   48;  Mismatches  137;  Indels   22;  Gaps    7;

Qy      8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
          |  ||     | | :|     :|:| : ||     : |   |:|||     |  | ||:||
Db      9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy     68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
          |  | : |  | ::|||      |   |  | :   :||| |:  | | :|:
Db     63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy    128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
          |: ::| | | |   |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db    121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy    188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
            | |||: ||  || |||  :   |:|:| | | |  |:        ||  : |:| |:
Db    181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy    247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
          |||  | :| ::  ||  || ||:|   |:   |    |  |              ||:|
Db    241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy    303 RHKSSFVI 310
          :  |||::
Db    292 KQTSSFLV 299


RESULT   3
US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (247)...(247)
;   NAME/KEY: UNSURE
;   LOCATION: (289)...(289)
US-09-188-930-189


  Query Match             25.2%;  Score 412;  DB 4;  Length 299;
  Best Local Similarity   32.1%;  Pred. No. 4.2e-34;
  Matches   99;  Conservative   48;  Mismatches  139;  Indels   22;  Gaps    7;

Qy      8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
          |  ||     | | :|     :|:| : ||     : |   |:|||     |  | ||:||
Db      9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy     68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
          |  | : |  | ::|||      |   |  | :   :||| |:  | | :|:
Db     63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy    128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
          |: ::| | | |   |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db    121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy    188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
            | |||: ||  || |||  :   |:|:| | | |  |:        ||  : |:| |:
Db    181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy    247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
          |||   :| ::  ||  || ||:|   |:   |    |  |              | :|
Db    241 AAVLVTXILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEXEF 291

Qy    303 RHKSSFVI 310
          :  |||::
Db    292 KQTSSFLV 299


RESULT   4
US-09-462-270-4
; Sequence 4, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
;  APPLICANT:  SmithKline Beecham Corporation
;  TITLE OF INVENTION:  Human F11 Antigen: A Cell Surface
;  TITLE OF INVENTION:  Receptor   Involved in Platelet Aggregation
;  FILE REFERENCE:  GH-70150US
;  CURRENT APPLICATION NUMBER: US/09/462,270
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/052,186
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-462-270-4


  Query Match             17.6%;  Score 288;  DB 4;  Length 205;
  Best Local Similarity   33.7%;  Pred. No. 1.2e-21;
  Matches   67;  Conservative   32;  Mismatches   92;  Indels    8;  Gaps    4;

Qy      8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
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Db      9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy     68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
          |  | : |  | ::|||      |   |  | :   :||| |:  | | :|:
Db     63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120
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Qy    128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
Db    121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy    188 PRFRNSSFHLNSETGTLVF 206
Db    181 RAFSNSSYVLNPTTGELVF 199


RESULT   5
US-08-597-495B-22
; Sequence 22, Application US/08597495B
; Patent No. 5712369
;  GENERAL INFORMATION:
;    APPLICANT:  Old, Lloyd J.;  Welt, Sydney; Ritter, Gerd;
;    APPLICANT:  Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;    APPLICANT:  Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;    APPLICANT:  Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;    TITLE OF INVENTION:  Colon Cell And Colon Cancer Cell
     TITLE OF INVENTION:  Associated Nucleic Acid Molecules, Protein And Peptides
     NUMBER OF SEQUENCES:  29
,    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/597,495B
;      FILING DATE:  02-Feb-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/511,876
;      FILING DATE:  04-Aug-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5712369man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5316.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
   INFORMATION FOR SEQ ID NO:  22:
     SEQUENCE CHARACTERISTICS:
       LENGTH:  319 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-597-495B-22


  Query Match             14.0%;  Score 228.5;  DB 1;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 2.7e-15;
  Matches   79;  Conservative   49;  Mismatches  128;  Indels   51;  Gaps   14;

Qy      29 IGAVNLKSSNRTPVVQEFESVELSCII-TDSQTSDPRIEWKKIQDEQTTYVF---FDNK- 83
Db      19 VDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKN 78

Qy      84 -IQGDL-------AGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTV 135
Db      79 YIHGELYKNRVSISNNAE-QSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLV 137

Qy     136 QVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDV-----PLPTDSRANPRF 190
Db     138 LVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQP-- 195

Qy     191 RNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE-EQEMEVYDLNIG---GII 246
Db     196 ------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIA 242

Qy     247 GGVLVVLAVLALITLGICCAYRRGYFIN--NKQDG----ESYKNPGKPDGVNYI--RTDE 298
Db     243 VGVVAALIIIGIIIYCCCC---RGKDDNTEDKEDARPNREAYEEP--PEQLRELSRERE 297

Qy     299 EGDFRHK 305
Db     298 EDDYRQE 304


RESULT   6
US-09-068-051A-22
; Sequence 22, Application US/09068051A
; Patent No. 6291235
;   GENERAL INFORMATION:
;        APPLICANT: Old, Lloyd J.;  Welt, Sydney; Ritter, Gerd;
;                   Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;                   Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;                   Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;        TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
;                            Associated Nucleic Acid Molecules, Protein And Peptides
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Wordperfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/068,051A
;             FILING DATE: 10-Dec-1998
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/597,495
;             FILING DATE: 02-Feb-1996
;             APPLICATION NUMBER: 08/511,876
;             FILING DATE: 04-Aug-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6291235man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5316.2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 22
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 319 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-068-051A-22


  Query Match             14.0%;  Score 228.5;  DB 4;  Length 319;
  Best Local Similarity   25.7%;  Pred. No. 2.7e-15;
  Matches   79;  Conservative   49;  Mismatches  128;  Indels   51;  Gaps   14;

Qy      29 IGAVNLKSSNRTPVVQEFESVELSCII-TDSQTSDPRIEWKKIQDEQTTYVF---FDNK- 83
Db      19 VDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKN 78

Qy      84 -IQGDL-------AGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTV 135
Db      79 YIHGELYKNRVSISNNAE-QSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLV 137

Qy     136 QVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDV-----PLPTDSRANPRF 190
```

```
          | |  | | :     :|    | ||  || | | ||| | ::     ||   :   |
Db    138 LVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQP-- 195

Qy    191 RNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE-EQEMEVYDLNIG---GII 246
                    :    :  | || | | :||: |:  |     :    :|:    ||
Db    196 ------------VSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIA 242

Qy    247 GGVLVVLAVLALITLGICCAYRRGYFIN--NKQDG----ESYKNPGKPDGVNYI--RTDE 298
           ||:  | :: :|    ||   ||   |  :|:|     |:|: |  |: :  :    :|
Db    243 VGVVAALIIIGIIIYCCCC---RGKDDNTEDKEDARPNREAYEEP--PEQLRELSRREE 297

Qy    299 EGDFRHK 305
          | |:| :
Db    298 EDDYRQE 304


RESULT   7
US-09-068-051A-32
; Sequence 32, Application US/09068051A
; Patent No. 6291235
; GENERAL INFORMATION:
;      APPLICANT: Old, Lloyd J.;  Welt, Sydney; Ritter, Gerd;
;                 Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
;                 Catimel, B.; Ji, Hong; Burgess, Anthony W.;
;                 Heath, Joan K.; White, Sara J.; Johnstone, Cameron
;      TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
;                          Associated Nucleic Acid Molecules, Protein And Peptides
;      NUMBER OF SEQUENCES: 33
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Fulbright & Jaworski LLP
;           STREET: 666 Fifth Avenue
;           CITY: New York City
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10103
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;           COMPUTER: IBM PS/2
;           OPERATING SYSTEM: PC-DOS
;           SOFTWARE: Wordperfect
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/068,051A
;           FILING DATE: 10-Dec-1998
;           CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/597,495
;           FILING DATE: 02-Feb-1996
;           APPLICATION NUMBER: 08/511,876
;           FILING DATE: 04-Aug-1995
;      ATTORNEY/AGENT INFORMATION:
;           NAME: Hanson, No. 6291235man D.
;           REGISTRATION NUMBER: 30,946
;           REFERENCE/DOCKET NUMBER: LUD 5316.2
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 318-3168
;           TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 32
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 318 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-068-051A-32


  Query Match           13.2%;  Score 215.5;  DB 4;  Length 318;
  Best Local Similarity   24.1%;  Pred. No. 5.8e-14;
  Matches   72;  Conservative   40;  Mismatches  114;  Indels   73;  Gaps   13;

Qy     48 SVELSCIITDSQTSDPR--IEWKKIQDEQT----------TYVF---FDNKIQGDLAGR 91
          || | |   ::  ||    |:| |:  ||          |::   ::|:::  ::
Db     37 SVTLPCTY-NTYVSDREGFIQWDKLLRSQTERVVTWNFVTKKYIYGNRYENRVR--VSND 93


Qy     92 AEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVP 151
          || |   |: |  :|  |:  | | |   :|:    :  : | | | |  | | :   :
Db     94 AE-LSNASITIDQLTMDDNGTYECSVSLMSDQDVNAKSRVRLLVLVPPSKPDCSIQGEMV 152

Qy    152 VGKMATLHCQESEGHPRPHYSW-----YRNDVPLPTDSRANPRFRNSSFHLNSETGTLVF 206
          :|    | |  :|| | | |||          ||       |                |:
Db    153 IGNNIQLTCHSAEGSPSPQYSWKSYNAQNQQRPLTQPVSGEP--------------LLL 197

Qy    207 TAVHKDDSGQYYCIASNDAGSARCE--------EQEMEVYDLNIGGIIGGVLVVLAVLAL 258
            :  : :| | | :||| |   |           : :|     || | | | | :: :
Db    198 KNISTETAGYYICTSSNDVGIESCNITVAPRPPSMNIALY----AGIAGSVFVALIIIGV 253

Qy    259 ITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYI-----------RTDEEGDFRHK 305
          |    ||          | | :  :   :|:   |             | ||: | ||:
Db    254 IVYCCCC--------REKDDKDQDREDARPNRAAYQVPKKEQKEISRGREDED-DHRHE 303


RESULT   8
US-09-175-928-2
; Sequence 2, Application US/09175928A
; Patent No. 6312921
; GENERAL INFORMATION:
;  APPLICANT: Jacobs, Kenneth
;  APPLICANT: McCoy, John M.
;  APPLICANT: LaVallie, Edward R.
;  APPLICANT: Collins-Racie, Lisa A.
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maurice
;  APPLICANT: Mi, Sha
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: 6006B.AJ172A
;  CURRENT APPLICATION NUMBER: US/09/175,928A
;  CURRENT FILING DATE: 1998-10-20
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-175-928-2


  Query Match           12.1%;  Score 197.5;  DB 4;  Length 387;
  Best Local Similarity   25.4%;  Pred. No. 5.4e-12;
  Matches   76;  Conservative   43;  Mismatches  119;  Indels   61;  Gaps   12;

Qy     18 FFLLLLFRGCLIGAVNLKSSNRTPVVQEF------ESVELSCIITDSQTSDPR--IEW-- 67
          |: : |   || | |::    :  :   |       :| | || | :  |  :  |:|
Db      5 FWKVFLILSCLAGQVSVV---QVTIPDGFVNVTVGSNVTLICIYTTTVASREQLSIQWSF 61

Qy     68 --KKIQDEQTTYVF----------FDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRC 115
            ||  :  : |            | ::| |     :   |  |: | ::   || :| |
Db     62 FHKKEMEPISIYFSQGGQAVAIGQFKDRITG-----SNDPGNASITISHMQPADSGIYIC 116

Qy    116 EVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYR 175
          :|    |    :: :: ::| |||  |:| |      |   :| |  : | | | | |::
Db    117 DVNNPPDFLGQNQGILNVSVLVKPSKPLCSVQGRPETGHTISLSCLSALGTPSPVYYWHK 176

Qy    176 ---NDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |: :|     ||            || ||   :   : | | | | |  |:: ||
Db    177 LEGRDI-VPVKENFNP----------TTGILVIGNLTNFEQGYYQCTAINRLGNSSCE- 223

Qy    233 QEMEVYDLNIG----GIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGK 287
                ||       ||| | |:   | | | : : |      |  ||   :: :   |
Db    224 -----IDLTSSHPEVGIIVGALIGSLVGAAIIISVVC------FARNKAKAKAKERNSK 271


RESULT   9
US-08-979-424-1
; Sequence 1, Application US/08979424
; Patent No. 5942606
```

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;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VIRAL RECEPTOR PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  390 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGFET03
;      CLONE:  1232054
US-08-979-424-1


  Query Match             10.4%;  Score 169.5;  DB 2;  Length 390;
  Best Local Similarity   26.3%;  Pred. No. 4e-09;
  Matches   77;  Conservative   37;  Mismatches  116;  Indels   63;  Gaps   14;

        2 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESV-----ELSCIIT 56
          ||  | | :|   ||                     :||   |:  | |      |   ::
Db     22 ALAPPSRAQLQLHLP-------------------ANRLQAVEGGEVVLPAWYTLHGEVS 61

Qy     57 DSQTSD-PRIEW----KKIQDEQTTYVFFDNKIQGDLAGRAEILG----KTSLKIWNVTR 107
           ||  : | : |    |: :|:  :|:   | :     | : :        ||::  :
Db     62 SSQPWEVPFVMWFFKQKEKEDQVLSYI---NGVTTSKPGVSLVYSMPSRNLSLRLEGLQE 118

Qy    108 RDSALYRCEV-VARNDRKEIDEIV--IELTVQVKPVTPVCRVPKAVPVGKMATLHCQESE 164
          :||  | | | |     |     :  :|| | | |  | ||:     ||   || ||
Db    119 KDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPR 178

Qy    165 GHPRPHYSWYRNDVPLPTDSRANPRFRNSSFH---LNSETGTLVFTAVHKDDSGQYYCIA 221
            |   | |           |  | |:  :|    |:   |:|  | :    :| | | |
Db    179 SKPAVQYQW----------DRQLPSFQ--TFFAPALDVIRGSLSLTNLSSSMAGVYVCKA 226

Qy    222 SNDAGSARCEEQEMEVYD----LNIGGIIGGVLVVLAVLALITLGICCAYRRG 270
           |: |:|:|    :||        : | : | || | :|| : |     :|||
Db    227 HNEVGTAQC-NVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVL---LYHRRG 275


RESULT  10
US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
;  GENERAL INFORMATION:
;    APPLICANT:  Robert W. Finberg, Jeffrey M. Bergelson,
;    APPLICANT:  and Marshall S. Horwitz
;    TITLE OF INVENTION:  CAR, A No. 6210921el Coxsackievirus and Adenovirus
;    TITLE OF INVENTION:  Receptor
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,383B
;      FILING DATE:  12-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,100
;      FILING DATE:  13-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  DFN-020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  365 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-928-383B-2


  Query Match             9.8%;  Score 160.5;  DB 4;  Length 365;
  Best Local Similarity   26.3%;  Pred. No. 3e-08;
  Matches   74;  Conservative   33;  Mismatches  123;  Indels   51;  Gaps   13;

Qy     21 LLLFRGCLIGAVNLKSSNRTPVVQEF------ESVELSCIITDS-QTSDP-RIEW----- 67
           |||     | | |:   |       :|       |:  | |  | | :   |  |||
Db      3 LLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA 62

Qy     68 --KKIQDEQTTYVFFDNKIQG----DLAGRAEIL------GKTSLKIWNVTRRDSALYRC 115
             :|:  :|   ::  :||      || ||          |  |: : |:   |   |:|
Db     63 DNQKV--DQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120

Qy    116 EVVARNDRKEIDEIV---IELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
          :|      |:   :    | | | |||    | |  :  :|    : |: ||      |
Db    121 KV------KKAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYE 174

Qy    173 WYR--NDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARC 230
          | :  :   :|| | |              :  :       : || | |   |  || :|
Db    175 WQKLSDSQKMPTSSLA----------EMTSSVISVKNASSEYSGTYSCTVRNRVGSDQC 223

Qy    231 EEQEMEVYDLNIGGIIGGVLV-VLAVLALITLGI-CCAYRR 269
            :   |   |  |:| | ::  |  |||| | | ||  :|
Db    224 LLRLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCCRKKR 264


RESULT  11
US-08-979-424-3
; Sequence 3, Application US/08979424
; Patent No. 5942606
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
```

```
;    TITLE OF INVENTION:  VIRAL RECEPTOR PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  365 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1946351
US-08-979-424-3


  Query Match             9.7%;  Score 159.5;  DB 2;  Length 365;
  Best Local Similarity   26.5%;  Pred. No. 3.8e-08;
  Matches   74;  Conservative   35;  Mismatches  123;  Indels   47;  Gaps   13;

Qy      21 LLLFRGCLIGAVNLKSSNRTPVVQEF------ESVELSCIITDS-QTSDP-RIEW----- 67
           |||    | | |:   |      :|       |: | |  | | :   |  |||
Db       3 LLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA 62

Qy      68 --KKIQDEQTTYVFFDNKIQG----DLAGRAEIL------GKTSLKIWNVTRRDSALYRC 115
             :|:  :|   ::  :||      || ||          |  |: : |:   |   |:|
Db      63 DNQKV--DQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120

Qy     116 EVVARNDRKEIDEIV---IELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
          :|      |:   :    | | | |||    | |  :  :|    : |:  ||     |
Db     121 KV------KKAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYE 174

Qy     173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
          | :      :||:  |    :|:     :  :       : || | |   |  || :|
Db     175 WQK-----LSDSQKMP----TSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLL 225

Qy     233 QEMEVYDLNIGGIIGGVLV-VLAVLALITLGI-CCAYRR 269
           :   |   |  |:| | ::  |  ||||  | | ||  :|
Db     226 RLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCCRKKR 264


RESULT  12
US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
;  APPLICANT: DeGregori, James
;  TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
;  FILE REFERENCE: 90-98
;  CURRENT APPLICATION NUMBER: US/09/272,496
;  CURRENT FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: US 60/092782
;  EARLIER FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-272-496-2


  Query Match             9.7%;  Score 159.5;  DB 4;  Length 365;
  Best Local Similarity   26.5%;  Pred. No. 3.8e-08;
  Matches   74;  Conservative   35;  Mismatches  123;  Indels   47;  Gaps   13;

Qy      21 LLLFRGCLIGAVNLKSSNRTPVVQEF------ESVELSCIITDS-QTSDP-RIEW----- 67
           |||    | | |:   |      :|       |: | |  | | :   |  |||
Db       3 LLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA 62

Qy      68 --KKIQDEQTTYVFFDNKIQG----DLAGRAEIL------GKTSLKIWNVTRRDSALYRC 115
             :|:  :|   ::  :||      || ||          |  |: : |:   |   |:|
Db      63 DNQKV--DQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120

Qy     116 EVVARNDRKEIDEIV---IELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
          :|      |:   :    | | | |||    | |  :  :|    : |:  ||     |
Db     121 KV------KKAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYE 174

Qy     173 WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
          | :      :||:  |    :|:     :  :       : || | |   |  || :|
Db     175 WQK-----LSDSQKMP----TSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLL 225

Qy     233 QEMEVYDLNIGGIIGGVLV-VLAVLALITLGI-CCAYRR 269
           :   |   |  |:| | ::  |  ||||  | | ||  :|
Db     226 RLNVVPPSNKAGLIAGAIIGTLLALALIGLIIFCCRKKR 264


RESULT  13
US-08-986-485-2
; Sequence 2, Application US/08986485
; Patent No. 6046030
; GENERAL INFORMATION:
;    APPLICANT:  WU, SHUJIAN
;    APPLICANT:  SWEET, RAYMOND
;    APPLICANT:  TRUNEH, ALEMSEGED
;    TITLE OF INVENTION:  A HUMAN LIG-1 HOMOLOG (HLIG-1)
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/986,485
;      FILING DATE:  08-DEC-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/059,448
;      FILING DATE:  22-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70264
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1101 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-986-485-2


  Query Match             9.6%;  Score 157.5;  DB 3;  Length 1101;
  Best Local Similarity   23.2%;  Pred. No. 3.1e-07;
  Matches   70;  Conservative   45;  Mismatches  120;  Indels   67;  Gaps   15;

Qy      34 LKSSNRTP---VVQEFESVELSCIITDSQTSDPRIEWKK-------IQDEQTTYVFFDNK 83
           | |  :||    ::       | |  |     :|:| |:|        .  |:  :|  |:
Db     606 LPSFTKTPHDITIRTTTVARLECAATGH--PNPQIAWQKDGGTDFPAARERRMHVMPDD- 662

Qy      84 IQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPV 143
                 ::   | :||      |: :| |   |:|    |      |||   |   |
Db     663 ---------DVFFITDVKI-----DDAGVYSC--TAQNSAGSISANA-TLTVLETPSLVV 705

Qy     144 CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGT 203
               : | ||:   | | :: |:| |  :|:: | ||    |          ||  :
Db     706 PLEDRVVSVGETVALQC-KATGNPPPRITWFKGDRPLSLTER---------HHLTPDNQL 755

Qy     204 LVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNI---------GGIIG--GVLVV 252
           ||   |  :|:|:| |  ||  |: |   |       |::         |  :|   : ||
Db     756 LVVQNVVAEDAGRYTCEMSNTLGTERAHSQ------LSVLPAAGCRKDGTTVGIFTIAVV 809

Qy     253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGK----PDGVNYIRTDEEGDFRHKSSF 308
            :::    : :|  |:       | :  |  |  :    ||  :|:    :|    :
Db     810 SSIVLTSLVWVCIIYQ----TRKKSEEYSVTNTDETVVPPDVPSYL--SSQGTLSDRQET 863

Qy     309 VI 310
           |:
Db     864 VV 865


RESULT  14
US-08-752-307B-11
; Sequence 11, Application US/08752307B
; Patent No. 5952171
;  GENERAL INFORMATION:
;    APPLICANT:  McCarthy, Sean A.
;    APPLICANT:  Gearing, David P.
;    APPLICANT:  Levinson, Douglas A.
;    TITLE OF INVENTION:  METHOD FOR IDENTIFYING GENES
;    TITLE OF INVENTION:  ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/752,307B
;      FILING DATE:  19-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meiklejohn, Ph.D., Anita L.
;      REGISTRATION NUMBER:  35,283
;      REFERENCE/DOCKET NUMBER:  09404/020001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  612 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-752-307B-11


  Query Match             9.5%;  Score 155.5;  DB 2;  Length 612;
  Best Local Similarity   30.2%;  Pred. No. 2.1e-07;
  Matches   60;  Conservative   21;  Mismatches   75;  Indels   43;  Gaps   10;

Qy      40 TPVVQEFESVE-------LSCIITDSQTSDPRIEWKKIQDE-QTTYVFFDNKIQGDLAGR 91
           ||:       ||       | ||      |  | | | |   |       ||:|
Db     248 TPMGSTSNKVELRGNVLLLECIAAGLPT--PVIRWIKEGGELPANRTFFEN--------- 296

Qy      92 AEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVP 151
                | :||| :|:  ||  |:|   |||         || :||:  |           :
Db     297 ----FKKTLKIIDVSEADSGNYKC--TARNTLGSTHH-VISVTVKAAPYWITAPRNLVLS 349

Qy     152 VGKMATLHCQESEGHPRPHYSWYRNDVPL---PTD-SRANPRFRNSSFHLNSETGTLVFT 207
             |:  || |: : |:|:|  ||  | ||:   | | ||                 :  |::|:
Db     350 PGEDGTLICR-ANGNPKPSISWLTNGVPIAIAPEDPSR------------KVDGDTIIFS 396

Qy     208 AVHKDDSGQYYCIASNDAG 226
           || :  |  | | |||: |
Db     397 AVQERSSAVYQCNASNEYG 415


RESULT  15
US-08-506-296B-28
; Sequence 28, Application US/08506296B
; Patent No. 6313265
;  GENERAL INFORMATION:
;    APPLICANT:  Phillips, Greg
;    APPLICANT:  Cunningham, Bruce A.
;    APPLICANT:  Crossin, Kathryn L.
;    TITLE OF INVENTION:  NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
;    TITLE OF INVENTION:  CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute
;      STREET:  10550 No. 6313265th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  U.S.
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/506,296B
;      FILING DATE:  24-JUL-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 488.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  1268 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-506-296B-28


  Query Match             9.5%;  Score 155.5;  DB 4;  Length 1268;
  Best Local Similarity   30.2%;  Pred. No. 6.2e-07;
  Matches   60;  Conservative   21;  Mismatches   75;  Indels   43;  Gaps   10;

Qy     40 TPVVQEFESVE-------LSCIITDSQTSDPRIEWKKIQDE-QTTYVFFDNKIQGDLAGR 91
          ||:      ||       | ||     |  | | | |   |      ||:|
Db    248 TPMGSTSNKVELRGNVLLLECIAAGLPT--PVIRWIKEGGELPANRTFFEN--------- 296

Qy     92 AEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVP 151
             | :||| :|:  ||  |:|   |||       || :||:  |             :
Db    297 ----FKKTLKIIDVSEADSGNYKC--TARNTLGSTHH-VISVTVKAAPYWITAPRNLVLS 349

Qy    152 VGKMATLHCQESEGHPRPHYSWYRNDVPL---PTD-SRANPRFRNSSFHLNSETGTLVFT 207
           |:  || |: : |:|:|  ||  | ||:   | | ||             :  |::|:
Db    350 PGEDGTLICR-ANGNPKPSISWLTNGVPIAIAPEDPSR-----------KVDGDTIIFS 396

Qy    208 AVHKDDSGQYYCIASNDAG 226
          || :  |  | | |||: |
Db    397 AVQERSSAVYQCNASNEYG 415


Search completed: September 19, 2002, 17:33:16
Job time: 234 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:40:17 ; Search time 30.81 Seconds
(without alignments)
966.819 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

[redacted] size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	290	2	I68750	MHC class I lympho
2	8	2.6	336	2	A86406	probable RING zinc
3	8	2.6	342	1	HLHUC4	MHC class I histoc
4	8	2.6	348	2	E82933	type I restriction
5	8	2.6	366	2	JH0546	class I histocompa
6	8	2.6	366	2	JH0547	class I histocompa
7	8	2.6	366	2	JH0545	class I histocompa
8	8	2.6	366	2	I37078	HLA-C alpha chain
9	8	2.6	492	2	AB1013	probable membrane
10	8	2.6	784	2	A86676	carbon starvation
11	7	2.3	77	2	JC5645	lymphotoxin beta -
12	7	2.3	113	2	AH1748	hypothetical prote
13	7	2.3	171	2	G70548	hypothetical prote
14	7	2.3	172	2	T08548	hypothetical prote
15	7	2.3	173	2	T01282	hypothetical prote
16	7	2.3	173	2	B90241	hypothetical prote
17	7	2.3	173	2	T25730	hypothetical prote
18	7	2.3	177	2	E85833	partial probable s
19	7	2.3	177	2	B90988	partial probable s
20	7	2.3	208	2	T03627	GTP-binding protei
21	7	2.3	208	2	T01588	GTP-binding protei
22	7	2.3	211	2	E86888	hypothetical prote
23	7	2.3	214	2	T47268	phosphatidylserine
24	7	2.3	217	2	T30446	occlusion-derived
25	7	2.3	242	2	G84315	cobalt transport p
26	7	2.3	244	2	A46066	lymphotoxin beta -
27	7	2.3	255	2	T35883	transcription regu
28	7	2.3	280	2	PH0269	epidermal autoanti
29	7	2.3	294	2	H84023	phosphate ABC tran
30	7	2.3	297	2	A81002	conserved hypothet
31	7	2.3	297	2	AB3037	hypothetical prote
32	7	2.3	299	2	A98249	nitrate transport
33	7	2.3	300	2	A82017	probable lipoprote
34	7	2.3	302	2	B70471	heat shock protein
35	7	2.3	306	2	I49139	lymphotoxin-beta -
36	7	2.3	314	2	C98193	sugar transport sy
37	7	2.3	314	2	AG3093	hypothetical prote
38	7	2.3	324	2	T27302	hypothetical prote
39	7	2.3	333	2	I38974	G protein-coupled
40	7	2.3	343	2	H95879	probable sugar ABC
41	7	2.3	346	2	D75303	conserved hypothet
42	7	2.3	362	2	G75614	GGDEF family prote
43	7	2.3	375	2	T46378	hypothetical prote
44	7	2.3	376	2	F71815	hypothetical prote
45	7	2.3	380	2	E88421	protein R74.2 [imp
46	7	2.3	382	2	T24963	hypothetical prote
47	7	2.3	391	2	E72539	hypothetical prote
48	7	2.3	392	1	RWHUPD	poliovirus recepto
49	7	2.3	392	2	B44194	poliovirus recepto
50	7	2.3	400	2	T24258	hypothetical prote
51	7	2.3	402	2	T04348	endosperm specific
52	7	2.3	402	2	G83367	hypothetical prote
53	7	2.3	403	1	GRECY	tyrosine-specific
54	7	2.3	403	2	G90955	tyrosine-specific
55	7	2.3	403	2	D85804	tyrosine-specific
56	7	2.3	417	1	RWHUPA	poliovirus recepto
57	7	2.3	417	2	A44194	poliovirus recepto
58	7	2.3	420	2	T36532	probable membrane
59	7	2.3	421	2	H86217	protein T27G7.16 [
60	7	2.3	431	2	D81282	probable efflux pr
61	7	2.3	437	2	AE1849	proton/sodium-glut
62	7	2.3	454	2	JC4616	apyrase (EC 3.6.1.
63	7	2.3	463	2	D84065	glucose-1-phosphat
64	7	2.3	481	2	S69808	lincomycin resista
65	7	2.3	490	2	A96556	probable tRNA-guan
66	7	2.3	491	1	O4RBPC	cytochrome P450 2B
67	7	2.3	491	2	S31277	cytochrome P450 2B
68	7	2.3	491	2	S31278	cytochrome P450 2B
69	7	2.3	491	2	S35666	cytochrome P450 2B
70	7	2.3	503	2	E83490	probable MFS trans
71	7	2.3	504	2	E87628	hypothetical prote
72	7	2.3	523	2	B95922	hypothetical nucle
73	7	2.3	524	2	A31318	glucose transporte
74	7	2.3	530	2	C95268	probable ABC trans
75	7	2.3	558	2	B87098	conserved hypothet

ALIGNMENTS

RESULT 1
I68750
MHC class I lymphocyte antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C;Accession: I68750
R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
A;Reference number: I54457; MUID:89233295
A;Accession: I68750
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-290 <RES>
A;Cross-references: GB:M28207; NID:g576478; PIDN:AAA53259.1; PID:g576479
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;144-209/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    249 VLVVLAVL 256
          ||||||||
Db    241 VLVVLAVL 248


RESULT   2
A86406
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86406
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: A86406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <STO>
A;Cross-references: GB:AE005172; NID:g11024872; PIDN:AAG26956.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1


  Query Match              2.6%;  Score 8;  DB 2;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    250 LVVLAVLA 257
          ||||||||
Db     28 LVVLAVLA 35


RESULT   3
HLHUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C;Accession: A24512
R;Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
iol. Chem. 260, 13414-13423, 1985
itle: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A;Reference number: A92500; MUID:86033791
A;Accession: A24512
A;Molecule type: DNA
A;Residues: 1-342 <DAV>
A;Cross-references: GB:M11886; NID:g184173; PIDN:AAA52665.1; PID:g386777
C;Genetics:
A;Gene: GDB:HLA-C
A;Cross-references: GDB:119311; OMIM:142840
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology <IMM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match              2.6%;  Score 8;  DB 1;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    249 VLVVLAVL 256
          ||||||||
Db    293 VLVVLAVL 300


RESULT   4
E82933
type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
A;Reference number: A82870
A;Accession: E82933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30504.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: hsdM-1; UU098
A;Genetic code: SGC3


  Query Match              2.6%;  Score 8;  DB 2;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    123 RKEIDEIV 130
          ||||||||
Db    336 RKEIDEIV 343


RESULT   5
JH0546
class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0546
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to huma
A;Reference number: JH0534; MUID:92078860
A;Accession: JH0546
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60249; NID:g22882; PIDN:CAA42801.1; PID:g22883
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status
F;25-114/Domain: alpha-1 <AL1>
F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-366/Domain: intracellular #status predicted <INT>


  Query Match              2.6%;  Score 8;  DB 2;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    249 VLVVLAVL 256
          ||||||||
Db    317 VLVVLAVL 324


RESULT   6
JH0547
class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:46:24 ; Search time 17.64 Seconds
(without alignments)
680.446 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	80	1	TX3A_PHONI	P81793 phoneutria
2	8	2.6	342	1	1CXX_HUMAN	P10321 homo sapien
3	8	2.6	366	1	1C02_GORGO	P30385 gorilla gor
4	8	2.6	366	1	1C03_GORGO	P30386 gorilla gor
5	8	2.6	366	1	1C04_GORGO	P30387 gorilla gor
6	8	2.6	366	1	1C11_HUMAN	Q29631 homo sapien
7	8	2.6	435	1	YGIK_SALTY	P40800 salmonella
8	7	2.3	224	1	XLR1_MOUSE	Q9z114 mus musculu
9	7	2.3	244	1	TNFC_HUMAN	Q06643 homo sapien
10	7	2.3	302	1	HTPX_AQUAE	O67798 aquifex aeo
11	7	2.3	306	1	TNFC_MOUSE	P41155 mus musculu
12	7	2.3	333	1	GPR8_HUMAN	P48146 homo sapien
13	7	2.3	343	1	HMD_METVO	Q50840 methanococc
14	7	2.3	403	1	TYRP_ECOLI	P18199 escherichia
15	7	2.3	417	1	PVR_CERAE	P32506 cercopithec
16	7	2.3	417	1	PVR_HUMAN	P15151 homo sapien
17	7	2.3	454	1	APY_SOLTU	P80595 solanum tub
18	7	2.3	481	1	LMRA_STRLN	P46104 streptomyce
19	7	2.3	491	1	CPB4_RABIT	P00178 oryctolagus
20	7	2.3	491	1	CPB5_RABIT	P12789 oryctolagus
21	7	2.3	524	1	GTR2_HUMAN	P11168 homo sapien
22	7	2.3	595	1	IF2P_ARCFU	O29490 archaeoglob
23	7	2.3	617	1	PYS1_PSEAE	Q06583 pseudomonas
24	7	2.3	643	1	PGT_HUMAN	Q92959 homo sapien
25	7	2.3	643	1	PGT_RAT	Q00910 rattus norv
26	7	2.3	688	1	PYS2_PSEAE	Q06584 pseudomonas
27	7	2.3	697	1	TGLC_CHICK	Q01841 gallus gall
28	7	2.3	721	1	YJIY_ECOLI	P39396 escherichia
29	7	2.3	758	1	SC18_YEAST	P18759 saccharomyc
30	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
31	7	2.3	981	1	SCA4_RICFE	Q9aj37 rickettsia
32	7	2.3	987	1	K6P1_CANAL	O94201 candida alb
33	7	2.3	991	1	SCA4_RICSI	Q9aj77 rickettsia
34	7	2.3	1011	1	SCA4_RICAF	Q9aj83 rickettsia
35	7	2.3	1011	1	SCA4_RICMN	Q9aj82 rickettsia
36	7	2.3	1012	1	SCA4_RICSL	Q9aj80 rickettsia
37	7	2.3	1013	1	SCA4_RICRH	Q9aj81 rickettsia
38	7	2.3	1018	1	SCA4_RICJA	Q9aj79 rickettsia
39	7	2.3	1022	1	SCA4_RICCN	Q52658 rickettsia
40	7	2.3	1053	1	ITA3_MOUSE	Q62470 mus musculu
41	7	2.3	1066	1	ITA3_CRISP	P17852 cricetidae
42	7	2.3	1066	1	ITA3_HUMAN	P26006 homo sapien
43	7	2.3	1105	1	YEGE_ECOLI	P38097 escherichia
44	7	2.3	1169	1	EX5B_BORBU	O51578 borrelia bu
45	7	2.3	1234	1	YNX5_CAEEL	P34578 caenorhabdi
46	7	2.3	4684	1	PLE1_HUMAN	Q15149 homo sapien
47	7	2.3	5065	1	EPPL_HUMAN	P58107 homo sapien
48	6	1.9	38	1	CRS3_NOTGO	P15534 nototodarus
49	6	1.9	46	1	LHA1_ECTHA	P80100 ectothiorho
50	6	1.9	57	1	ANDP_DROME	P21663 drosophila
51	6	1.9	57	1	YI60_ARCFU	O28419 archaeoglob
52	6	1.9	61	1	RS14_MYCGA	O52345 mycoplasma
53	6	1.9	64	1	YDT6_SCHPO	O14211 schizosacch
54	6	1.9	74	1	SRP_SOYBN	Q07502 glycine max
55	6	1.9	76	1	SECG_BACSU	O32233 bacillus su
56	6	1.9	82	1	TX32_PHONI	O76201 phoneutria
57	6	1.9	83	1	TX31_PHONI	O76200 phoneutria
58	6	1.9	86	1	PTHP_STRMU	P45596 streptococc
59	6	1.9	87	1	PTHP_BACHD	Q9k8d2 bacillus ha
60	6	1.9	87	1	PTHP_STRBO	Q9wxk8 streptococc
61	6	1.9	87	1	PTHP_STRSL	P24366 streptococc
62	6	1.9	94	1	YE23_HAEIN	P44194 haemophilus
63	6	1.9	96	1	FER1_AQUAE	O67065 aquifex aeo
64	6	1.9	99	1	YO10_BPHP1	P51712 bacteriopha
65	6	1.9	102	1	KCRB_PIG	Q29594 sus scrofa
66	6	1.9	109	1	V42_BPT3	P20316 bacteriopha
67	6	1.9	115	1	NRG4_MOUSE	Q9wtx4 mus musculu
68	6	1.9	115	1	TKN1_RABIT	P41540 oryctolagus
69	6	1.9	118	1	YKD7_YEAST	P32858 saccharomyc
70	6	1.9	119	1	B2MG_HUMAN	P01884 homo sapien
71	6	1.9	119	1	B2MG_PONPY	P16213 pongo pygma
72	6	1.9	123	1	Y055_MYCGE	P47301 mycoplasma
73	6	1.9	125	1	FRDD_MYCTU	Q10763 mycobacteri
74	6	1.9	130	1	DHSC_PARDE	Q59659 paracoccus
75	6	1.9	130	1	KV5G_MOUSE	P01639 mus musculu

ALIGNMENTS

```
RESULT   1
TX3A_PHONI
ID   TX3A_PHONI     STANDARD;      PRT;    80 AA.
AC   P81793;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Neurotoxin Pn3A precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99053416; PubMed=9839681;
RA   Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.F.,
RA   Cordeiro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,
RA   Gomez M.V., Beirao P.S.L.;
RT   "Cloning, cDNA sequence analysis and patch clamp studies of a toxin
RT   from the venom of the armed spider (Phoneutria nigriventer).";
RL   Toxicon 36:1971-1980(1998).
CC   -!- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Produced by the venomous gland.
CC   -!- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.
```

```
DR   InterPro; IPR004169; spidertoxin.
DR   Pfam; PF02819; spidertoxin; 1.
KW   Calcium channel inhibitor; Toxin; Neurotoxin; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     37       POTENTIAL.
FT   CHAIN        38     71       NEUROTOXIN PN3A.
FT   PROPEP       72     80       POTENTIAL.
SQ   SEQUENCE   80 AA;  8937 MW;  B5BF209257EB6793 CRC64;


  Query Match             2.6%;  Score 8;  DB 1;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 0.98;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     256 LALITLGI 263
           ||||||||
Db      12 LALITLGI 19


[redacted]LT   2
[redacted]_HUMAN
ID   1CXX_HUMAN     STANDARD;      PRT;   342 AA.
AC   P10321;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   HLA class I histocompatibility antigen, C-4 alpha chain.
GN   HLA-C OR HLAC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86033791; PubMed=3863816;
RA   Davidson W.F., Kress M., Khoury G., Jay G.;
RT   "Comparison of HLA class I gene sequences. Derivation of
RT   locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
RT   HLA-C genes.";
RL   J. Biol. Chem. 260:13414-13423(1985).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC       THE IMMUNE SYSTEM.
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M11886; AAA52665.1; -.
DR   PIR; A24512; HLHUC4.
DR   HSSP; P30685; 1A9B.
DR   MIM; 142840; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein.
FT   DOMAIN       25     90       EXTRACELLULAR ALPHA-1.
FT   DOMAIN       91    182       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      183    274       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      275    284       CONNECTING PEPTIDE.
FT   TRANSMEM    285    309
FT   DOMAIN      310    342       CYTOPLASMIC TAIL.
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    164    203       BY SIMILARITY.
SQ   SEQUENCE   342 AA;  38082 MW;  22C39A6D84C05D09 CRC64;


  Query Match             2.6%;  Score 8;  DB 1;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     249 VLVVLAVL 256
           ||||||||
Db     293 VLVVLAVL 300


RESULT   3
1C02_GORGO
ID   1C02_GORGO     STANDARD;      PRT;   366 AA.
AC   P30385;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Class I histocompatibility antigen, GOGO-C0201 alpha chain precursor.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC       THE IMMUNE SYSTEM.
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60251; CAA42803.1; -.
DR   PIR; JH0545; JH0545.
DR   HSSP; P30685; 1A9B.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    366       CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                GOGO-C0201 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    333
FT   DOMAIN      334    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   366 AA;  40954 MW;  05E159364C769FC5 CRC64;


  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:44:45 ; Search time 48.09 Seconds
(without alignments)
1115.168 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	4	Q9BX67	Q9bx67 homo sapien
2	208	67.1	309	4	Q96FL1	Q96fl1 homo sapien
3	32	10.3	310	11	Q9D8B7	Q9d8b7 mus musculu
4	28	9.0	310	11	Q9EPK4	Q9epk4 mus musculu
5	28	9.0	310	11	Q9D1M9	Q9d1m9 mus musculu
6	8	2.6	39	7	Q9TNT2	Q9tnt2 homo sapien
7	8	2.6	80	5	P81793	P81793 phoneutria
8	8	2.6	125	11	Q9CS62	Q9cs62 mus musculu
9	8	2.6	233	10	Q9LR49	Q9lr49 arabidopsis
10	8	2.6	246	5	Q966C0	Q966c0 caenorhabdi
11	8	2.6	290	7	Q29990	Q29990 homo sapien
12	8	2.6	294	16	Q98EQ9	Q98eq9 rhizobium l
13	8	2.6	309	5	Q9N4Y9	Q9n4y9 caenorhabdi
14	8	2.6	313	7	Q9MY31	Q9my31 homo sapien
15	8	2.6	322	2	Q9RPI7	Q9rpi7 desulfitoba
16	8	2.6	336	10	Q9C7E9	Q9c7e9 arabidopsis
17	8	2.6	338	7	Q9MXL5	Q9mxl5 pan troglod
18	8	2.6	348	7	Q9MWJ9	Q9mwj9 gorilla gor
19	8	2.6	348	16	Q9PR46	Q9pr46 ureaplasma
20	8	2.6	363	7	Q95HC2	Q95hc2 homo sapien
21	8	2.6	365	7	Q9XRX8	Q9xrx8 pongo pygma
22	8	2.6	365	7	Q9XRX7	Q9xrx7 pongo pygma
23	8	2.6	365	7	Q9MXG4	Q9mxg4 pan troglod
24	8	2.6	366	6	O46684	O46684 pan troglod
25	8	2.6	366	7	Q9TPL2	Q9tpl2 pan troglod
26	8	2.6	366	7	Q9MXD2	Q9mxd2 pan troglod
27	8	2.6	366	7	Q95603	Q95603 homo sapien
28	8	2.6	366	7	Q95463	Q95463 homo sapien
29	8	2.6	366	7	Q29865	Q29865 homo sapien
30	8	2.6	366	7	O78083	O78083 homo sapien
31	8	2.6	366	7	Q9TQP9	Q9tqp9 homo sapien
32	8	2.6	366	7	Q29652	Q29652 homo sapien
33	8	2.6	366	7	O19617	O19617 homo sapien
34	8	2.6	784	16	Q9CIF4	Q9cif4 lactococcus
35	8	2.6	1290	13	Q9W6E1	Q9w6e1 gallus gall
36	7	2.3	77	4	P78370	P78370 homo sapien
37	7	2.3	85	12	Q99GX8	Q99gx8 heliocoverp
38	7	2.3	113	16	Q928J9	Q928j9 listeria in
39	7	2.3	146	17	Q973F7	Q973f7 sulfolobus
40	7	2.3	158	2	Q9EWB3	Q9ewb3 streptomyce
41	7	2.3	161	2	Q9FBK8	Q9fbk8 streptomyce
42	7	2.3	171	16	O06422	O06422 mycobacteri
43	7	2.3	172	10	Q9SZQ8	Q9szq8 arabidopsis
44	7	2.3	173	5	Q22966	Q22966 caenorhabdi
45	7	2.3	173	10	O64567	O64567 arabidopsis
46	7	2.3	173	17	Q97ZK3	Q97zk3 sulfolobus
47	7	2.3	177	16	Q931Y0	Q931y0 staphylococ
48	7	2.3	179	2	Q9RKC2	Q9rkc2 streptomyce
49	7	2.3	191	10	Q9XHM2	Q9xhm2 medicago tr
50	7	2.3	202	6	Q9TUF5	Q9tuf5 cercopithec
51	7	2.3	202	6	Q9TUF4	Q9tuf4 propithecus
52	7	2.3	208	10	O80501	O80501 arabidopsis
53	7	2.3	208	10	Q40525	Q40525 nicotiana t
54	7	2.3	211	16	Q9CDV2	Q9cdv2 lactococcus
55	7	2.3	214	2	O32618	O32618 helicobacte
56	7	2.3	214	6	O62722	O62722 oryctolagus
57	7	2.3	217	12	Q9YMN1	Q9ymn1 lymantria d
58	7	2.3	224	11	Q9R1M6	Q9r1m6 mus musculu
59	7	2.3	227	12	Q91BE2	Q91be2 spodoptera
60	7	2.3	242	17	Q9HPH6	Q9hph6 halobacteri
61	7	2.3	242	17	Q96XA1	Q96xa1 sulfolobus
62	7	2.3	247	4	O75192	O75192 homo sapien
63	7	2.3	255	2	O50521	O50521 streptomyce
64	7	2.3	267	3	Q9Y7B2	Q9y7b2 emericella
65	7	2.3	275	16	Q92NE9	Q92ne9 rhizobium m
66	7	2.3	277	11	P70361	P70361 mus musculu
67	7	2.3	280	9	Q9XJ89	Q9xj89 bacteriopha
68	7	2.3	286	2	Q9EWQ5	Q9ewq5 streptomyce
69	7	2.3	292	10	Q9SE74	Q9se74 brassica ca
70	7	2.3	294	10	Q9SE75	Q9se75 brassica ol
71	7	2.3	294	16	Q9K8L4	Q9k8l4 bacillus ha
72	7	2.3	297	16	Q9JXB2	Q9jxb2 neisseria m
73	7	2.3	300	16	Q9JWV3	Q9jwv3 neisseria m
74	7	2.3	306	16	Q92K19	Q92k19 rhizobium m
75	7	2.3	310	11	Q9JM11	Q9jm11 marmota mon

ALIGNMENTS

RESULT 1
Q9BX67
ID Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE JUNCTIONAL ADHESION MOLECULE 3 PRECURSOR (JUNCTIONAL ADHESION
DE MOLECULE-2).

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GN   JAM-2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Cunningham S.A., Arrate M.P., Tran T.M.;
RT   "Cloning of Human Junctional Adhesion Molecule 3.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT   "Heterogeneity of endothelial junctions is reflected by differential
RT   expression and specific subcellular localization of the three JAM
RT   family members.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
     Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
     "Junctional adhesion molecules (JAMs) and interendothelial
     junctions.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;


  Query Match             100.0%;  Score 310;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy     301 DFRHKSSFVI 310
          ||||||||||
Db     301 DFRHKSSFVI 310


RESULT   2
Q96FL1
ID   Q96FL1      PRELIMINARY;      PRT;   309 AA.
AC   Q96FL1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR IMAGE:3875338) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EYE, AND RETINOBLASTOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010690; AAH10690.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   309 AA;  34917 MW;  50C5B1B7872E8DF3 CRC64;


  Query Match             67.1%;  Score 208;  DB 4;  Length 309;
  Best Local Similarity   99.7%;  Pred. No. 2.2e-204;
  Matches  308;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS 61
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Db       1 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS 60

Qy      62 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 120

Qy     122 DRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 181
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 180

Qy     182 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240

Qy     242 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 301
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Db     241 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 300

Qy     302 FRHKSSFVI 310
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Db     301 FRHKSSFVI 309


RESULT   3
Q9D8B7
ID   Q9D8B7      PRELIMINARY;      PRT;   310 AA.
AC   Q9D8B7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1110002N23RIK PROTEIN.
GN   JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:39:08 ; Search time 52.83 Seconds
(without alignments)
651.767 Million cell updates/sec

Title: US-09-524-531C-15
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	21	AAB27276	Human confluency r
2	310	100.0	310	21	AAB33457	Human PRO1868 prot
3	310	100.0	310	21	AAY96735	PRO1868, an A33 an
4	310	100.0	310	22	AAM93323	Human polypeptide,
5	310	100.0	310	22	AAM93905	Human polypeptide,
6	310	100.0	310	22	AAU12440	Human PRO1868 poly
7	310	100.0	310	22	AAB80272	Human PRO1868 prot
8	310	100.0	310	22	AAB80383	Secreted protein e
9	310	100.0	310	22	AAB80408	Secreted protein e
10	310	100.0	310	22	AAB80409	Secreted protein e
11	310	100.0	311	21	AAB38333	Human secreted pro
12	310	100.0	311	21	AAB38383	Human secreted pro
13	310	100.0	311	21	AAB38384	Human secreted pro
14	310	100.0	339	22	AAB80431	Gene #13 associate
15	209	67.4	310	21	AAY96294	Human IGFAM-6 immu
16	161	51.9	285	21	AAB39254	Human secreted pro
17	151	48.7	291	22	ABG04645	Novel human diagno
18	151	48.7	404	22	ABG12109	Novel human diagno
19	104	33.5	361	22	ABG22401	Novel human diagno
20	89	28.7	89	20	AAY11472	Human 5' EST secre
21	63	20.3	267	22	ABG27038	Novel human diagno
22	51	16.5	264	22	ABG07157	Novel human diagno
23	51	16.5	301	22	ABG22399	Novel human diagno
24	38	12.3	68	22	ABG22398	Novel human diagno
25	24	7.7	310	21	AAB27272	Human confluency r
26	24	7.7	310	21	AAB27278	Murine confluency
27	8	2.6	31	22	ABB29193	Peptide #1844 enco
28	8	2.6	31	22	ABB34350	Peptide #1856 enco
29	8	2.6	31	22	ABB19769	Protein #1768 enco
30	8	2.6	31	22	AAM55147	Human brain expres
31	8	2.6	31	22	AAM67540	Human bone marrow
32	8	2.6	31	22	AAM15353	Peptide #1787 enco
33	8	2.6	31	22	AAM27831	Peptide #1868 enco
34	8	2.6	31	22	AAM03112	Peptide #1794 enco
35	8	2.6	120	21	AAG30027	Arabidopsis thalia
36	8	2.6	154	21	AAG30026	Arabidopsis thalia
37	8	2.6	190	21	AAG30025	Arabidopsis thalia
38	7	2.3	7	21	AAB27269	Murine CRAM-1 tyro
39	7	2.3	12	16	AAR83341	Kb-binding random
40	7	2.3	14	16	AAR83451	Arabidopsis thalia
41	7	2.3	39	21	AAB44378	Human secreted pro
42	7	2.3	39	22	ABB31269	Peptide #3920 enco
43	7	2.3	39	22	ABB36477	Peptide #3983 enco
44	7	2.3	39	22	ABB21819	Protein #3818 enco
45	7	2.3	39	22	AAM57241	Human brain expres
46	7	2.3	39	22	AAM69641	Human bone marrow
47	7	2.3	39	22	AAM17457	Peptide #3891 enco
48	7	2.3	39	22	AAM29977	Peptide #4014 enco
49	7	2.3	39	22	AAM05134	Peptide #3816 enco
50	7	2.3	40	22	AAG74530	Human colon cancer
51	7	2.3	56	22	AAO04488	Human polypeptide
52	7	2.3	58	22	AAU49383	Propionibacterium
53	7	2.3	67	21	AAG34555	Arabidopsis thalia
54	7	2.3	70	21	AAG34554	Arabidopsis thalia
55	7	2.3	71	22	AAO11264	Human polypeptide
56	7	2.3	73	22	AAU39482	Propionibacterium
57	7	2.3	78	22	ABG29189	Novel human diagno
58	7	2.3	87	22	AAU19792	Human novel extrac
59	7	2.3	89	21	AAG00327	Human secreted pro
60	7	2.3	92	21	AAG59054	Arabidopsis thalia
61	7	2.3	92	21	AAG60335	Arabidopsis thalia
62	7	2.3	102	20	AAY73830	Human prostate tum
63	7	2.3	104	22	AAO09976	Human polypeptide
64	7	2.3	106	22	AAGB2299	S. epidermidis ope
65	7	2.3	110	21	AAG59053	Arabidopsis thalia
66	7	2.3	110	21	AAG60334	Arabidopsis thalia
67	7	2.3	127	22	ABG04070	Novel human diagno
68	7	2.3	135	21	AAG03799	Human secreted pro
69	7	2.3	149	20	AAY38777	Neisseria meningit
70	7	2.3	152	21	AAG58379	Arabidopsis thalia
71	7	2.3	158	21	AAG06039	Arabidopsis thalia
72	7	2.3	162	18	AAW20313	H. pylori surface
73	7	2.3	172	21	AAG16659	Arabidopsis thalia
74	7	2.3	173	21	AAG58378	Arabidopsis thalia
75	7	2.3	175	21	AAG16658	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAB27276
ID AAB27276 standard; Protein; 310 AA.
XX

```
AC   AAB27276;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Human confluency regulated adhesion molecule 1 #2.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
XX
PR   11-MAR-1999;   99EP-0200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
DR   N-PSDB; AAA95306.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Claim 2; Fig 6; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing.
XX
SQ   Sequence   310 AA;


  Query Match             100.0%;  Score 310;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Db        1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy       61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Qy      121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db      121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy      181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Qy      241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Qy      301 DFRHKSSFVI 310
            ||||||||||
Db      301 dfrhkssfvi 310


RESULT   2
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ID   AAB33457 standard; Protein; 310 AA.
XX
AC   AAB33457;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
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XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
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DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58622.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 88; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   310 AA;


  Query Match             100.0%;  Score 310;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310


RESULT   3
AAY96735
ID   AAY96735 standard; Protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Signal_peptide
FT   Modified-site   26..31
FT                   /note= "N-myristoylation site"
FT   Modified-site   69..77
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   104..107
FT                   /note= "N-glycosylation site"
FT   Modified-site   106..109
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   107..110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                     phosphorylation site"
FT   Modified-site   192..195
FT                   /note= "N-glycosylation site"
FT   Modified-site   215..220
FT                   /note= "N-myristoylation site"
FT   Modified-site   226..231
FT                   /note= "N-myristoylation site"
FT   Domain          243..263
FT                   /label= Transmembrane_domain
FT   Modified-site   243..248
FT                   /note= "N-myristoylation site"
FT   Modified-site   244..249
FT                   /note= "N-myristoylation site"
FT   Modified-site   262..267
FT                   /note= "N-myristoylation site"
FT   Modified-site   296..299
FT                   /note= "Casein kinase II phosphorylation site"
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US28634.
XX
PR   16-DEC-1998;   98US-0112851.
PR   16-DEC-1998;   98US-0113145.
PR   22-DEC-1998;   98US-0113511.
PR   12-JAN-1999;   99US-0115558.
PR   12-JAN-1999;   99US-0115565.
PR   12-JAN-1999;   99US-0115733.
PR   09-FEB-1999;   99US-0119341.
PR   10-FEB-1999;   99US-0119537.
PR   12-FEB-1999;   99US-0119965.
PR   02-JUN-1999;   99WO-US12252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51265.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide
XX
PS   Claim 1; Fig 14; 154pp; English.
XX
CC   This is PRO1868, a putative homologue of A33 antigen, a known
CC   colorectal cancer-associated marker. The invention concerns novel
CC   secreted and transmembrane proteins, designated PRO polypeptides. The
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CC   cDNA and gene sequences are useful in the recombinant production of PRO
CC   polypeptides, as a hybridization probe to screen libraries to isolate
CC   cDNAs with sequence identity to PRO polypeptides or to map the gene
CC   encoding the PRO polypeptides and analyzing genetic disorders. The
CC   cDNA/gene can also be used to produce transgenic animals useful for the
CC   development and screening of therapeutically useful reagents. They can
CC   also be used in gene therapy, e.g. to replace a defective gene.
XX
SQ   Sequence   310 AA;


  Query Match           100.0%;  Score 310;  DB 21;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT   4
AAM93323
ID   AAM93323 standard; Protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94243.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 2845; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is a polypeptide
CC   encoded by a full length human cDNA of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence   310 AA;


  Query Match           100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT   5
AAM93905
ID   AAM93905 standard; Protein; 310 AA.
XX
AC   AAM93905;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 4051.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
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PA  (HELI-) HELIX RES INST.
XX
PI  Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI  Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR  WPI; 2001-524255/58.
DR  N-PSDB; AAK94867.
XX
PT  830 Primers useful for synthesizing full length cDNA clones and their
PT  use in genetic manipulation -
XX
PS  Claim 8; SEQ ID NO 4051; 1380pp + sequence listing; English.
XX
CC  The invention relates to primers for synthesising full length cDNA
CC  clones. 830 cDNA molecules encoding a human protein have been
CC  isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC  molecules have been determined. Primers for synthesising the full length
CC  cDNA are useful for clarifying the function of the protein encoded by
CC  the cDNA. The full length clones were obtained by construction of full
CC  length enriched cDNA libraries that were synthesised by the oligo-capping
CC  method. The primers enable the production of the full length cDNA easily
CC  without any special methods. The present sequence is a polypeptide
CC  encoded by a full length human cDNA of the invention.
CC  Note: The sequence data for this patent did not form part of the printed
CC  specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ  Sequence   310 AA;


  Query Match             100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

       241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310


RESULT   6
AAU12440
ID  AAU12440 standard; Protein; 310 AA.
XX
AC  AAU12440;
XX
DT  24-OCT-2001  (first entry)
XX
DE  Human PRO1868 polypeptide sequence.
XX
KW  Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW  breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW  cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW  adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS  Homo sapiens.
XX
PN  WO200140466-A2.
XX
PD  07-JUN-2001.
XX
PF  01-DEC-2000; 2000WO-US32678.
XX
PR  01-DEC-1999;   99WO-US28301.
PR  01-DEC-1999;   99WO-US28634.
PR  02-DEC-1999;   99WO-US28551.
PR  02-DEC-1999;   99WO-US28564.
PR  02-DEC-1999;   99WO-US28565.
PR  09-DEC-1999;   99US-0170262.
PR  16-DEC-1999;   99WO-US30095.
PR  20-DEC-1999;   99WO-US30911.
PR  20-DEC-1999;   99WO-US30999.
PR  30-DEC-1999;   99WO-US31243.
PR  06-JAN-2000; 2000WO-US00277.
PR  06-JAN-2000; 2000WO-US00376.
PR  11-FEB-2000; 2000WO-US03565.
PR  18-FEB-2000; 2000WO-US04341.
PR  18-FEB-2000; 2000WO-US04342.
PR  22-FEB-2000; 2000WO-US04414.
PR  24-FEB-2000; 2000WO-US04914.
PR  24-FEB-2000; 2000WO-US05004.
PR  01-MAR-2000; 2000WO-US05601.
PR  20-MAR-2000; 2000WO-US07377.
PR  21-MAR-2000; 2000WO-US07532.
PR  30-MAR-2000; 2000WO-US08439.
PR  17-MAY-2000; 2000WO-US13705.
PR  22-MAY-2000; 2000WO-US14042.
PR  30-MAY-2000; 2000WO-US14941.
PR  02-JUN-2000; 2000WO-US15264.
PR  10-NOV-2000; 2000WO-US30873.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI  Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI  Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR  WPI; 2001-408281/43.
DR  N-PSDB; AAS21512.
XX
PT  Isolated, secretory and transmembrane PRO polypeptide used to detect
PT  other PRO polypeptides, link bioactive molecules to cells expressing
PT  PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT  lung, breast, prostate, cervical -
XX
PS  Claim 12; Fig 538; 813pp; English.
XX
CC  AAU12172-AAU12446 represent novel human secretory and transmembrane
CC  PRO polypeptides. The PRO polypeptides are useful to detect other
CC  PRO polypeptides, to link bioactive molecules to cells expressing
CC  PRO polypeptides, to modulate biological activities of cells expressing
CC  PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC  breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC  polypeptide expression in a cell sample to that in a control sample.
CC  Some of the 275 sequences are also useful to stimulate the release of
CC  tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC  proliferation or differentiation of chondrocytes, the proliferation or
CC  gene expression in pericyte cells, the release of proteoglycans from
CC  cartilage, the proliferation of inner ear utricular supporting cells or
CC  of T-lymphocytes, the release of a cytokine from peripheral blood
CC  monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC  the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC  skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC  to factor VIIA. The PRO polypeptides can be used in assays to identify
CC  molecules involved in binding interactions. The polynucleotides encoding
CC  PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC  transgenic or knock out animals and can be used in gene therapy.
XX
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```
SQ   Sequence   310 AA;

  Query Match           100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT   7
AAB80272
ID   AAB80272 standard; Protein; 310 AA.
XX
AC   AAB80272;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human PRO1868 protein.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
PF   22-FEB-2000; 2000WO-US04414.
XX
PR   07-JUL-1999;   99US-0143048.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000;   99WO-US00219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N;
PI   Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ,  Kljavin IJ;
PI   Mather JP,  Pan J,  Paoni NF,  Roy MA,  Stewart TA,  Tumas D;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-081051/09.
DR   N-PSDB; AAF72433.
XX
PT   Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT   the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT   squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT   Alzheimer's disease) -
XX
PS   Claim 1; Fig 124; 393pp; English.
XX
CC   The present sequence is one of sixty one novel secreted and
CC   transmembrane PRO polypeptides. The PRO polypeptides are
CC   useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC   squamous cell carcinoma), gastrointestinal disorders (e.g.
CC   enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC   Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC   endometrial bleeding angiogenesis, ischaemias such as coronary
CC   ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC   rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC   diabetes and retinal disorders such as retinitis pigmentosum.
CC   The PRO nucleic acids have applications in molecular biology, including
CC   use as hybridization probes, and in chromosome and gene mapping.
XX
SQ   Sequence   310 AA;

  Query Match           100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT   8
AAB80383
ID   AAB80383 standard; protein; 310 AA.
XX
AC   AAB80383;
XX
DT   24-APR-2001  (first entry)
XX
DE   Secreted protein encoded by gene #13.
XX
KW   Secreted protein; human; autoimmune; hyperproliferation;
```

```
KW  cardiovascular; cerebrovascular; infection; food.
XX
OS  Homo sapiens.
XX
PN  WO200107459-A1.
XX
PD  01-FEB-2001.
XX
PF  20-JUL-2000; 2000WO-US19735.
XX
PR  23-JUL-1999;  99US-0145220.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI  Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR  WPI; 2001-123261/13.
XX
PT  New isolated nucleic acid encoding 29 secreted proteins, for
PT  diagnosing, preventing and treating e.g. autoimmune,
PT  hyperproliferative, cardiovascular, and ocular diseases or disorders
PT  and microorganism infections -
XX
PS  Claim 11; Page 538-539; 601pp; English.
XX
CC  The present invention relates to 29 human secreted proteins. The
CC  invention is used to prevent autoimmune diseases e.g. rheumatoid
CC  arthritis, hyperproliferative disorders e.g. neoplasms of the
CC  breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC  cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC  nervous system disorders e.g. Alzheimer's disease, infections
CC  caused by bacteria, viruses and fungi and ocular disorders e.g.
CC  corneal infection. Also used in food preparations.
XX
SQ  Sequence  310 AA;


  Query Match            100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT  9
AAB80408
ID  AAB80408 standard; protein; 310 AA.
XX
AC  AAB80408;
XX
DT  24-APR-2001  (first entry)
XX
DE  Secreted protein encoded by gene #38.
XX
KW  Secreted protein; human; autoimmune; hyperproliferation;
KW  cardiovascular; cerebrovascular; infection; food.
XX
OS  Homo sapiens.
XX
PN  WO200107459-A1.
XX
PD  01-FEB-2001.
XX
PF  20-JUL-2000; 2000WO-US19735.
XX
PR  23-JUL-1999;  99US-0145220.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI  Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR  WPI; 2001-123261/13.
XX
PT  New isolated nucleic acid encoding 29 secreted proteins, for
PT  diagnosing, preventing and treating e.g. autoimmune,
PT  hyperproliferative, cardiovascular, and ocular diseases or disorders
PT  and microorganism infections -
XX
PS  Claim 11; Page 557-558; 601pp; English.
XX
CC  The present invention relates to 29 human secreted proteins. The
CC  invention is used to prevent autoimmune diseases e.g. rheumatoid
CC  arthritis, hyperproliferative disorders e.g. neoplasms of the
CC  breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC  cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC  nervous system disorders e.g. Alzheimer's disease, infections
CC  caused by bacteria, viruses and fungi and ocular disorders e.g.
CC  corneal infection. Also used in food preparations.
XX
SQ  Sequence  310 AA;


  Query Match            100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy     61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy    121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy    181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy    241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy    301 DFRHKSSFVI 310
          ||||||||||
Db    301 dfrhkssfvi 310


RESULT  10
```

```
AAB80409
ID   AAB80409 standard; protein; 310 AA.
XX
AC   AAB80409;
XX
DT   24-APR-2001  (first entry)
XX
DE   Secreted protein encoded by gene #39.
XX
KW   Secreted protein; human; autoimmune; hyperproliferation;
KW   cardiovascular; cerebrovascular; infection; food.
XX
OS   Homo sapiens.
XX
PN   WO200107459-A1.
XX
PD   01-FEB-2001.
XX
PF   20-JUL-2000; 2000WO-US19735.
XX
PR   23-JUL-1999;   99US-0145220.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Ebner R,  Duan RD,  Ni J,  Soppet DR,  Moore PA;
PI   Shi Y,  Lafleur DW,  Olsen HS,  Birse CE,  Komatsoulis GA;
XX
DR   WPI; 2001-123261/13.
XX
PT   New isolated nucleic acid encoding 29 secreted proteins, for
PT   diagnosing, preventing and treating e.g. autoimmune,
PT   hyperproliferative, cardiovascular, and ocular diseases or disorders
PT   and microorganism infections  -
XX
PS   Claim 11; Page 559-560; 601pp; English.
XX
CC   The present invention relates to 29 human secreted proteins. The
CC   invention is used to prevent autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the
CC   breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC   cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC   nervous system disorders e.g. Alzheimer's disease, infections
CC   caused by bacteria, viruses and fungi and ocular disorders e.g.
CC   corneal infection. Also used in food preparations.
XX
SQ   Sequence   310 AA;

  Query Match            100.0%;  Score 310;  DB 22;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310


RESULT  11
AAB38333
ID   AAB38333 standard; Protein; 311 AA.
XX
AC   AAB38333;
XX
DT   31-JAN-2001  (first entry)
XX
DE   Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW   Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW   cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW   nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW   vulnerary; gene therapy; infection; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200061623-A1.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US08979.
XX
PR   09-APR-1999;   99US-0128693.
PR   26-APR-1999;   99US-0130991.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Komatsoulis GA,  Rosen CA,  Soppet DR,  Shi Y;
PI   Lafleur DW,  Olsen HS,  Ebner R,  Florence KA,  Moore PA,  Birse CE;
PI   Young PE;
XX
DR   WPI; 2000-647418/62.
XX
PT   New nucleic acid molecules encoding 62 human secreted proteins for
PT   diagnosing, preventing, treating or ameliorating medical conditions and
PT   used as food additives or preservatives -
XX
PS   Claim 11; Page 603-604; 716pp; English.
XX
CC   Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC   human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC   and proteins are useful for preventing, ameliorating or treating medical
CC   conditions, e.g. by protein or gene therapy. The genes are isolated from
CC   a range of human tissues disclosed in the specification. The nucleic
CC   acids, proteins, antibodies and (ant)agonists are useful in the
CC   diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC   rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC   of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC   arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC   angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC   infections caused by bacteria, viruses and fungi; and (h) ocular
CC   disorders e.g. corneal infection. The polypeptides can also be used to
CC   aid wound healing and epithelial cell proliferation, to prevent skin
CC   aging due to sunburn, to maintain organs before transplantation, for
CC   supporting cell culture of primary tissues, to regenerate tissues and in
CC   chemotaxis.
XX
SQ   Sequence   311 AA;

  Query Match            100.0%;  Score 310;  DB 21;  Length 311;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60
```

```
Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310
```

RESULT 12
AAB38383
ID AAB38383 standard; Protein; 311 AA.
XX
AC AAB38383;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW vulnerary; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200061623-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08979.
XX
PR 09-APR-1999; 99US-0128693.
PR 26-APR-1999; 99US-0130991.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;
XX
DR WPI; 2000-647418/62.
XX
PT New nucleic acid molecules encoding 62 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 11; Page 642-643; 716pp; English.
XX
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.
XX
SQ Sequence 311 AA;

```
  Query Match             100.0%;  Score 310;  DB 21;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-295;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310
```

RESULT 13
AAB38384
ID AAB38384 standard; Protein; 311 AA.
XX
AC AAB38384;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW vulnerary; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200061623-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08979.
XX
PR 09-APR-1999; 99US-0128693.
PR 26-APR-1999; 99US-0130991.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;
XX
DR WPI; 2000-647418/62.
XX
PT New nucleic acid molecules encoding 62 human secreted proteins for

PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 11; Page 643-644; 716pp; English.
XX
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 310; DB 21; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.7e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310
```

RESULT 14
AAB80431
ID AAB80431 standard; peptide; 339 AA.
XX
AC AAB80431;
XX
DT 24-APR-2001 (first entry)
XX
DE Gene #13 associated peptide #1.
XX
KW Secreted protein; human; autoimmune; hyperproliferation;
KW cardiovascular; cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US19735.
XX
PR 23-JUL-1999; 99US-0145220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections -
XX
PS Disclosure; Page 75; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 310; DB 22; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 89

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 149

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 209

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ptdsranprfrnssfhlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 269

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     270 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 329

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     330 dfrhkssfvi 339
```

RESULT 15
AAY96294
ID AAY96294 standard; protein; 310 AA.
XX
AC AAY96294;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-6 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= signal_peptide
FT   Protein         31..310
FT                   /label= IGFAM-6
FT   Domain          46..117
FT                   /label= Ig_domain
FT   Domain          153..221
FT                   /label= Ig_domain
FT   Domain          238..260
FT                   /label= transmembrane_domain
XX
PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27566.
XX
PR   19-NOV-1998;   99US-0113635.
PR   22-DEC-1998;   98US-0113635.
PR   07-APR-1999;   99US-0128194.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI; 2000-387796/33.
DR   N-PSDB; AAA27386.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders
PT   -
XX
PS   Claim 1; Page 82-83; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-6. Its gene was isolated from a cDNA library of leg
CC   tissue. It is expressed in reproductive, nervous and
CC   cardiovascular tissue, where cancer and inflammation are common. The
CC   gene, protein, its antibodies, agonists and antagonists are suitable for
CC   diagnosing and treating many diseases, including cancer, immune system
CC   disorders (such as inflammation, AIDS, allergies, anaemia,
CC   arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC   disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
     multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
     systemic lupus erythematosus and ulcerative colitis), complications of
     cancer, haemodialysis and extracorporeal circulation, trauma and
CC   haematopoietic cancer (such as leukaemia) and infections caused by
CC   bacteria, viruses, fungi or parasites.
XX
SQ   Sequence   310 AA;


  Query Match             67.4%;  Score 209;  DB 21;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 1.8e-196;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdlagraeilgktslkiwnvtrrdsalyrcevvar 120

Qy     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkeideivieltvqvkpvtpvcrvpkavpvgkmatlhcqeseghprphyswyrndvpl 180

Qy     181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfrnssshlnsetgtlvftavhkddsgqyyciasndagsarceeqemevydl 240

Qy     241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtdeeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310


RESULT  16
AAB39254
ID   AAB39254 standard; Protein; 285 AA.
XX
AC   AAB39254;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
XX
KW   Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW   antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW   nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW   opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis;
KW   hyperproliferative disorder; cardiovascular disorder; infection;
KW   cerebrovascular disorder; nervous system disorder; ocular disorder;
KW   wound healing; chemotaxis.
XX
OS   Homo sapiens.
XX
PN   WO200056754-A1.
XX
PD   28-SEP-2000.
XX
PF   16-MAR-2000; 2000WO-US06792.
XX
PR   19-MAR-1999;   99US-0125362.
PR   10-DEC-1999;   99US-0169980.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen GA,  Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-579483/54.
DR   N-PSDB; AAC74237.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition  -
XX
PS   Disclosure; Page 32; 434pp; English.
XX
CC   The polynucleotide sequences given in AAC74223-C74279 encode the human
CC   secreted proteins represented in AAB39179-B39226. Sequences
CC   AAB39227-B39308 are alternative proteins encoded by the genes, and also
CC   protein sequences with which they share homology. The proteins have
CC   activities based on the tissues and cells in which they are expressed.
CC   Examples of activities include: immunosuppressive; antiarthritic;
CC   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
CC   fungicide; and opthalmalogical. The human secreted proteins,
CC   polynucleotides, antagonists and agonists of the invention may be useful
CC   in the treatment, prevention, and/or diagnosis of various disease,
CC   disorders and conditions such as autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC   also be used to aid wound healing and epithelial cell proliferation, to
CC   regenerate tissues, maintain organs before transplantation, in
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CC   chemotaxis and as a food additive or preservative e.g. to increase
CC   storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
CC   during the isolation and characterisation of the genes of the invention.
XX
SQ   Sequence   285 AA;


  Query Match             51.9%;  Score 161;  DB 21;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2e-149;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     150 VPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAV 209
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 vpvgkmatlhcqeseghprphyswyrndvplptdsranprfrnssfhlnsetgtlvftav 184

Qy     210 HKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRR 269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 hkddsgqyyciasndagsarceeqemevydlniggiiggvlvvlavlalitlgiccayrr 244

Qy     270 GYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
           |||||||||||||||||||||||||||||||||||||||||
Db     245 gyfinnkqdgesyknpgkpdgvnyirtdeegdfrhkssfvi 285


RESULT  17
ABG04645
ID   ABG04645 standard; Protein; 291 AA.
XX
AC   ABG04645;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #4636.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS68832.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 35004; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   291 AA;


  Query Match             48.7%;  Score 151;  DB 22;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-139;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      87 DLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRV 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 dlagraeilgktslkiwnvtrrdsalyrcevvarndrkeideivieltvqvkpvtpvcrv 193

Qy     147 PKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVF 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 pkavpvgkmatlhcqeseghprphyswyrndvplptdsranprfrnssfhlnsetgtlvf 253

Qy     207 TAVHKDDSGQYYCIASNDAGSARCEEQEMEV 237
           |||||||||||||||||||||||||||||||
Db     254 tavhkddsgqyyciasndagsarceeqemev 284


RESULT  18
ABG12109
ID   ABG12109 standard; Protein; 404 AA.
XX
AC   ABG12109;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #12100.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS76296.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 42468; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
```

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 404 AA;

Query Match 48.7%; Score 151; DB 22; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e-139;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 DLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRV 146
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 134 dlagraeilgktslkiwnvtrrdsalyrcevvarndrkeideivieltvqvkpvtpvcrv 193

Qy 147 PKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVF 206
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194 pkavpvgkmatlhcqeseghprphyswyrndvplptdsranprfrnssfhlnsetgtlvf 253

Qy 207 TAVHKDDSGQYYCIASNDAGSARCEEQEMEV 237
|||||||||||||||||||||||||||||||
Db 254 tavhkddsgqyyciasndagsarceeqemev 284

RESULT 19
ABG22401
ID ABG22401 standard; Protein; 361 AA.
XX
AC ABG22401;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22392.
XX
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86588.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52760; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 361 AA;

Query Match 33.5%; Score 104; DB 22; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.9e-93;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 GCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQ 85
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 35 gcligavnlkssnrtpvvqefesvelsciitdsqtsdpriewkkiqdeqttyvffdnkiq 94

Qy 86 GDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEI 129
|||||||||||||||||||||||||||||||||||||||||||||
Db 95 gdlagraeilgktslkiwnvtrrdsalyrcevvarndrkeidei 138

RESULT 20
AAY11472
ID AAY11472 standard; Protein; 89 AA.
XX
AC AAY11472;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID No 294.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9906551-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB01235.
XX
PR 01-AUG-1997; 97US-0905133.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI; 1999-153781/13.

```
DR   N-PSDB; AAX39538.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 34; Page 394; 434pp; English.
XX
CC   AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence   89 AA;


  Query Match             28.7%;  Score 89;  DB 20;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-79;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 malrrpprlrlcarlpdfflllfrgcligavnlkssnrtpvvqefesvelsciitdsqt 60

Qy      61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLA 89
           |||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdeqttyvffdnkiqgdla 89


RESULT  21
ABG27038
ID   ABG27038 standard; Protein; 267 AA.
XX
AC   ABG27038;

     18-FEB-2002  (first entry)

DE   Novel human diagnostic protein #27029.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS91225.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 57397; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   267 AA;


  Query Match             20.3%;  Score 63;  DB 22;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-53;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     239 DLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDE 298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 dlniggiiggvlvvlavlalitlgiccayrrgyfinnkqdgesyknpgkpdgvnyirtde 189

Qy     299 EGD 301
           |||
Db     190 egd 192


RESULT  22
ABG07157
ID   ABG07157 standard; Protein; 264 AA.
XX
AC   ABG07157;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #7148.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
```

DR WPI; 2001-639362/73.
DR N-PSDB; AAS71344.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 37516; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 264 AA;

Query Match 16.5%; Score 51; DB 22; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 GDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQ 136
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 214 gdlagraeilgktslkiwnvtrrdsalyrcevvarndrkeideivieltvq 264

RESULT 23
ABG22399
ID ABG22399 standard; Protein; 301 AA.
XX
ABG22399;

18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22390.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86586.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52758; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 301 AA;

Query Match 16.5%; Score 51; DB 22; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 GDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQ 136
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 214 gdlagraeilgktslkiwnvtrrdsalyrcevvarndrkeideivieltvq 264

RESULT 24
ABG22398
ID ABG22398 standard; Protein; 68 AA.
XX
AC ABG22398;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22389.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86585.

```
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 52757; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;


  Query Match             12.3%;  Score 38;  DB 22;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-29;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      49 VELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQG 86
           ||||||||||||||||||||||||||||||||||||||
Db      28 velsciitdsqtsdpriewkkiqdeqttyvffdnkiqg 65


RESULT  25
AAB27272
ID   AAB27272 standard; Protein; 310 AA.
XX
AC   AAB27272;

     23-FEB-2001  (first entry)

DE   Human confluency regulated adhesion molecule 1 #1.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
XX
PR   11-MAR-1999;   99EP-0200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Claim 1; Fig 3; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer,
CC   inflammation, to modulate cell-cell interactions and angiogenesis, and
CC   in the modulation of wound healing.
XX
SQ   Sequence   310 AA;


  Query Match             7.7%;  Score 24;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-15;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 PRPHYSWYRNDVPLPTDSRANPRF 190
           ||||||||||||||||||||||||
Db     167 prphyswyrndvplptdsranprf 190


RESULT  26
AAB27278
ID   AAB27278 standard; Protein; 310 AA.
XX
AC   AAB27278;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Murine confluency regulated adhesion molecule 1.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; mouse;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Mus sp.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
XX
PR   11-MAR-1999;   99EP-0200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
DR   N-PSDB; AAA97189.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Example; Fig 8; 59pp; English.
XX
CC   The present sequence is the murine confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing.
XX
SQ   Sequence   310 AA;


  Query Match             7.7%;  Score 24;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-15;
```

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    167 PRPHYSWYRNDVPLPTDSRANPRF 190
          |||||||||||||||||||||||||
Db    167 prphyswyrndvplptdsranprf 190
```

RESULT 27
ABB29193
ID ABB29193 standard; Peptide; 31 AA.
XX
AC ABB29193;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1844 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 27; SEQ ID NO 12161; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    249 VLVVLAVL 256
          ||||||||
Db     10 vlvvlavl 17
```

RESULT 28
ABB34350
ID ABB34350 standard; Peptide; 31 AA.
XX
AC ABB34350;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #1856 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 27; SEQ ID NO 26985; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    249 VLVVLAVL 256
          ||||||||
Db     10 vlvvlavl 17
```

RESULT 29
ABB19769
ID ABB19769 standard; Protein; 31 AA.
XX
AC ABB19769;

XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #1768 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15; SEQ ID No 21539; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
||||||||
Db 10 vlvvlavl 17

RESULT 30
AAM55147
ID AAM55147 standard; Protein; 31 AA.
XX
AC AAM55147;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27252.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 27252; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 31 AA;

Query Match 2.6%; Score 8; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
||||||||
Db 10 vlvvlavl 17

RESULT 31
AAM67540
ID AAM67540 standard; Protein; 31 AA.
XX
AC AAM67540;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27846.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.

GenCore version 4.5

OM protein - protein search, using sw model

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Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	2.3	14	2	US-08-310-912A-190	Sequence 190, App
2	7	2.3	14	4	US-09-301-085-190	Sequence 190, App
3	7	2.3	14	5	PCT-US95-04589-190	Sequence 190, App
4	7	2.3	52	4	US-09-330-330-9	Sequence 9, Appli
5	7	2.3	241	1	US-08-484-272-2	Sequence 2, Appli
6	7	2.3	241	1	US-08-476-489-2	Sequence 2, Appli
7	7	2.3	241	1	US-08-467-070-2	Sequence 2, Appli
8	7	2.3	241	1	US-08-467-070A-2	Sequence 2, Appli
9	7	2.3	241	5	PCT-US93-11669-2	Sequence 2, Appli
10	7	2.3	244	4	US-08-883-086-9	Sequence 9, Appli
11	7	2.3	249	2	US-09-154-802-1	Sequence 1, Appli
12	7	2.3	249	3	US-09-373-029-1	Sequence 1, Appli
13	7	2.3	333	1	US-08-148-215A-4	Sequence 4, Appli
14	7	2.3	454	4	US-09-240-639-11	Sequence 11, Appl
15	7	2.3	524	2	US-08-928-692-12	Sequence 12, Appl
16	7	2.3	642	1	US-08-706-936-2	Sequence 2, Appli
17	7	2.3	642	1	US-08-706-936-3	Sequence 3, Appli
18	7	2.3	643	2	US-08-616-844-39	Sequence 39, Appl
19	7	2.3	643	2	US-08-599-654-39	Sequence 39, Appl
20	7	2.3	643	3	US-08-944-868A-39	Sequence 39, Appl
21	7	2.3	643	3	US-08-944-423A-39	Sequence 39, Appl
22	7	2.3	643	3	US-08-944-496-39	Sequence 39, Appl
23	7	2.3	693	1	US-08-553-279-2	Sequence 2, Appli
24	7	2.3	885	2	US-08-310-912A-2	Sequence 2, Appli
25	7	2.3	885	3	US-08-841-089-2	Sequence 2, Appli
26	7	2.3	885	4	US-09-301-085-2	Sequence 2, Appli
27	7	2.3	885	5	PCT-US95-04570-2	Sequence 2, Appli
28	7	2.3	885	5	PCT-US95-04589-2	Sequence 2, Appli
29	7	2.3	907	3	US-08-930-996A-7	Sequence 7, Appli
30	7	2.3	909	2	US-08-310-912A-142	Sequence 142, App
31	7	2.3	909	4	US-09-301-085-142	Sequence 142, App
32	7	2.3	909	5	PCT-US95-04589-142	Sequence 142, App
33	7	2.3	4551	3	US-09-320-878-1	Sequence 1, Appli
34	7	2.3	4613	4	US-09-105-537-31	Sequence 31, Appl
35	7	2.3	11877	4	US-09-105-537-6	Sequence 6, Appli
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39	6	1.9	27	4	US-09-227-357-276	Sequence 276, App
40	6	1.9	39	4	US-09-220-528-49	Sequence 49, Appl
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42	6	1.9	45	4	US-09-085-761A-77	Sequence 77, Appl
43	6	1.9	50	1	US-08-331-394-12	Sequence 12, Appl
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46	6	1.9	50	2	US-08-744-139-12	Sequence 12, Appl
47	6	1.9	50	5	PCT-US95-06639-12	Sequence 12, Appl
48	6	1.9	51	2	US-08-691-814B-19	Sequence 19, Appl
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53	6	1.9	76	3	US-08-775-414-22	Sequence 22, Appl
54	6	1.9	76	4	US-08-931-858E-22	Sequence 22, Appl
55	6	1.9	76	4	US-08-981-739-22	Sequence 22, Appl
56	6	1.9	95	1	US-08-519-777-24	Sequence 24, Appl
57	6	1.9	95	1	US-08-742-035-24	Sequence 24, Appl
58	6	1.9	95	2	US-08-777-019-24	Sequence 24, Appl
59	6	1.9	95	2	US-08-777-143-24	Sequence 24, Appl
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61	6	1.9	95	4	US-08-931-858E-24	Sequence 24, Appl
62	6	1.9	95	4	US-08-981-739-24	Sequence 24, Appl
63	6	1.9	98	1	US-08-118-270-330	Sequence 330, App
64	6	1.9	98	5	PCT-US93-08528-330	Sequence 330, App
65	6	1.9	100	4	US-09-230-196-5	Sequence 5, Appli
66	6	1.9	106	4	US-08-936-165A-482	Sequence 482, App
67	6	1.9	111	4	US-09-220-528-53	Sequence 53, Appl
68	6	1.9	115	2	US-08-672-345C-18	Sequence 18, Appl
69	6	1.9	115	2	US-08-672-345C-108	Sequence 108, App
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71	6	1.9	115	4	US-09-214-095D-98	Sequence 98, Appl
72	6	1.9	119	1	US-08-469-486-49	Sequence 49, Appl
73	6	1.9	119	2	US-08-469-658-49	Sequence 49, Appl
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ALIGNMENTS

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; Sequence 190, Application US/08310912A
; Patent No. 5981730
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  208
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
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;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02110-2904
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/310,912A
;       FILING DATE:  September 22, 1994
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/227,360
;       FILING DATE:  April 13, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lech, Karen F.
;       REGISTRATION NUMBER:  35,238
;       REFERENCE/DOCKET NUMBER:  00786/254001
      TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  100254
;   INFORMATION FOR SEQ ID NO:  190:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  14 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-310-912A-190


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  Best Local Similarity   100.0%;  Pred. No. 5.8;
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Qy     256 LALITLG 262
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Db       5 LALITLG 11


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; Sequence 190, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
;  APPLICANT: Ausubel, Frederick M.
;  APPLICANT: Staskawicz, Brian J.
;  APPLICANT: Brent, Andrew F.
;  APPLICANT: Dahlbeck, Douglas
;  APPLICANT: Katagiri, Fumiaki
;  APPLICANT: Kunkel, Barbara N.
;  APPLICANT: Mindrinos, Michael N.
;  APPLICANT: Yu, Guo-Liang
;  TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
;  TITLE OF INVENTION: DETECTION  METHODS
;  FILE REFERENCE: 00786/254002
;  CURRENT APPLICATION NUMBER: US/09/301,085
;  CURRENT FILING DATE: 1999-04-28
;  EARLIER APPLICATION NUMBER: 08/310,912
;  EARLIER FILING DATE: 1994-09-22
;  EARLIER APPLICATION NUMBER: 08/227,360
;  EARLIER FILING DATE: 1994-04-13
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-301-085-190


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Qy     256 LALITLG 262
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Db       5 LALITLG 11


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; Sequence 190, Application PC/TUS9504589
;  GENERAL INFORMATION:
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Staskawicz, Brian J.
;    APPLICANT:  Brent, Andrew F.
;    APPLICANT:  Dahlbeck, Douglas
;    APPLICANT:  Katagiri, Fumiaki
;    APPLICANT:  Kunkel, Barbara N.
;    APPLICANT:  Mindrinos, Michael N.
;    APPLICANT:  Yu, Guo-Liang
;    TITLE OF INVENTION:  RPS2 GENE AND USES THEREOF
;    NUMBER OF SEQUENCES:  201
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2904
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04589
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,360
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/230001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  100254
;  INFORMATION FOR SEQ ID NO:  190:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-04589-190


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Qy     256 LALITLG 262
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Db       5 LALITLG 11


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; Sequence 9, Application US/09330330
; Patent No. 6274789
;  GENERAL INFORMATION:
;    APPLICANT:  Yano, Masahiro
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GenCore version 4.5

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Run on: September 19, 2002, 17:32:32 ; Search time 52.83 Seconds
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Perfect score: 310
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	21	AAB27272	Human confluency r
2	310	100.0	310	21	AAB27278	Murine confluency
3	24	7.7	285	21	AAB39254	Human secreted pro
4	24	7.7	291	22	ABG04645	Novel human diagno
5	24	7.7	310	21	AAB27276	Human confluency r
6	24	7.7	310	21	AAB33457	Human PRO1868 prot
7	24	7.7	310	21	AAY96735	PRO1868, an A33 an
8	24	7.7	310	21	AAY96294	Human IGFAM-6 immu
9	24	7.7	310	22	AAM93323	Human polypeptide,
10	24	7.7	310	22	AAM93905	Human polypeptide,
11	24	7.7	310	22	AAU12440	Human PRO1868 poly
12	24	7.7	310	22	AAB80272	Human PRO1868 prot
13	24	7.7	310	22	AAB80383	Secreted protein e
14	24	7.7	310	22	AAB80408	Secreted protein e
15	24	7.7	310	22	AAB80409	Secreted protein e
16	24	7.7	311	21	AAB38333	Human secreted pro
17	24	7.7	311	21	AAB38383	Human secreted pro
18	24	7.7	311	21	AAB38384	Human secreted pro
19	24	7.7	339	22	AAB80431	Gene #13 associate
20	24	7.7	404	22	ABG12109	Novel human diagno
21	21	6.8	361	22	ABG22401	Novel human diagno
22	15	4.8	68	22	ABG22398	Novel human diagno
23	15	4.8	89	20	AAY11472	Human 5' EST secre
24	10	3.2	267	22	ABG27038	Novel human diagno
25	8	2.6	48	17	AAW01191	Serine protease Pf
26	8	2.6	48	22	AAB50588	Flea serine protea
27	8	2.6	204	22	AAG81659	S. epidermidis ope
28	8	2.6	204	22	AAG82062	S. epidermidis ope
29	8	2.6	246	19	AAW41974	Flea serine protea
30	8	2.6	246	22	AAB50616	Flea serine protea
31	8	2.6	324	22	AAG93112	C glutamicum prote
32	8	2.6	324	22	AAB79609	Corynebacterium gl
33	8	2.6	336	22	AAU00245	L. maculans resist
34	8	2.6	506	21	AAG29349	Arabidopsis thalia
35	7	2.3	7	21	AAB27269	Murine CRAM-1 tyro
36	7	2.3	7	21	AAB27270	Murine CRAM-1 tyro
37	7	2.3	39	21	AAB44378	Human secreted pro
38	7	2.3	40	22	AAG74530	Human colon cancer
39	7	2.3	56	22	AAO04488	Human polypeptide
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41	7	2.3	67	21	AAG34555	Arabidopsis thalia
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44	7	2.3	85	20	AAY12629	Human 5' EST secre
45	7	2.3	91	22	AAG74654	Human colon cancer
46	7	2.3	92	21	AAG59054	Arabidopsis thalia
47	7	2.3	92	21	AAG60335	Arabidopsis thalia
48	7	2.3	93	22	AAU57205	Propionibacterium
49	7	2.3	101	22	AAU62010	Propionibacterium
50	7	2.3	104	22	AAO09976	Human polypeptide
51	7	2.3	110	21	AAG59053	Arabidopsis thalia
52	7	2.3	110	21	AAG60334	Arabidopsis thalia
53	7	2.3	111	22	AAU39287	Propionibacterium
54	7	2.3	115	22	ABG12822	Novel human diagno
55	7	2.3	121	21	AAB07727	Protein encoded by
56	7	2.3	127	22	ABG04070	Novel human diagno
57	7	2.3	145	21	AAY87479	Human chorionic go
58	7	2.3	147	21	AAG26119	Zea mays protein f
59	7	2.3	147	22	ABB70048	Drosophila melanog
60	7	2.3	158	21	AAG06039	Arabidopsis thalia
61	7	2.3	170	21	AAY78114	Human cytokine sig
62	7	2.3	170	22	AAB67667	Amino acid sequenc
63	7	2.3	173	22	ABB12245	Human CKSR-2 homol
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65	7	2.3	180	22	AAG81557	S. epidermidis ope
66	7	2.3	185	22	ABB52473	Escherichia coli p
67	7	2.3	201	22	AAG73773	Human colon cancer
68	7	2.3	208	21	AAG06037	Arabidopsis thalia
69	7	2.3	209	22	AAM23936	Human EST encoded
70	7	2.3	209	22	AAM23951	Human EST encoded
71	7	2.3	233	20	AAY27767	Human secreted pro
72	7	2.3	242	22	ABB30277	Peptide #2928 enco
73	7	2.3	242	22	ABB35443	Peptide #2949 enco
74	7	2.3	242	22	ABB20882	Protein #2881 enco
75	7	2.3	242	22	AAM56266	Human brain expres

ALIGNMENTS

RESULT 1
AAB27272
ID AAB27272 standard; Protein; 310 AA.
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AC   AAB27272;
XX
DT   23-FEB-2001  (first entry)
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DE   Human confluency regulated adhesion molecule 1 #1.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
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OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
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PR   11-MAR-1999;   99EP-0200746.
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PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Claim 1; Fig 3; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer,
CC   inflammation, to modulate cell-cell interactions and angiogenesis, and
CC   in the modulation of wound healing.
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SQ   Sequence   310 AA;


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Qy     121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
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Qy     181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
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Qy     301 DFRHKSSFVI 310
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Db     301 dfrhkssfvi 310


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AC   AAB27278;
XX
DT   23-FEB-2001  (first entry)
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DE   Murine confluency regulated adhesion molecule 1.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; mouse;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Mus sp.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
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PR   11-MAR-1999;   99EP-0200746.
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PA   (RMFD-) RMF DICTAGENE SA.
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PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
DR   N-PSDB; AAA97189.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Example; Fig 8; 59pp; English.
XX
CC   The present sequence is the murine confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing.
XX
SQ   Sequence   310 AA;


  Query Match             100.0%;  Score 310;  DB 21;  Length 310;
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Db       1 malsrrlrlrlyarlphfflllfrgcmieavnlkssnrnpvvhefesvelsciithsqt 60

Qy      61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdpriewkkiqdgqttyvyfdnkiqgdlagrtdvfgktslriwnvtrsdsaiyrcevval 120

Qy     121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ndrkevdeitielivqvkpvtpvcripaavpvgktatlqcqesegyprphyswyrndvpl 180

Qy     181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ptdsranprfqnssfhvnsetgtlvfnavhkddsgqyyciasndagaarcegqdmevydl 240

Qy     241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 niagiiggvlvvlivlavitmgiccayrrgcfisskqdgesykspgkhdgvnyirtseeg 300

Qy     301 DFRHKSSFVI 310
           ||||||||||
Db     301 dfrhkssfvi 310
```

RESULT 3
AAB39254
ID AAB39254 standard; Protein; 285 AA.
XX
AC AAB39254;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;
KW opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis;
KW hyperproliferative disorder; cardiovascular disorder; infection;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; chemotaxis.
XX
OS Homo sapiens.
XX
PN WO200056754-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US06792.
XX
PR 19-MAR-1999; 99US-0125362.
PR 10-DEC-1999; 99US-0169980.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen GA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-579483/54.
DR N-PSDB; AAC74237.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; Page 32; 434pp; English.
XX
CC The polynucleotide sequences given in AAC74223-C74279 encode the human
CC secreted proteins represented in AAB39179-B39226. Sequences
CC AAB39227-B39308 are alternative proteins encoded by the genes, and also
CC protein sequences with which they share homology. The proteins have
CC activities based on the tissues and cells in which they are expressed.
CC Examples of activities include: immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
fungicide; and opthalmalogical. The human secreted proteins,
CC polynucleotides, antagonists and agonists of the invention may be useful
CC in the treatment, prevention, and/or diagnosis of various disease,
CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC regenerate tissues, maintain organs before transplantation, in
CC chemotaxis and as a food additive or preservative e.g. to increase
CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
CC during the isolation and characterisation of the genes of the invention.
XX
SQ Sequence 285 AA;

Query Match 7.7%; Score 24; DB 21; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 142 prphyswyrndvplptdsranprf 165

RESULT 4
ABG04645
ID ABG04645 standard; Protein; 291 AA.
XX
AC ABG04645;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #4636.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS68832.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 35004; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 291 AA;

Query Match 7.7%; Score 24; DB 22; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||

```
Db    214 prphyswyrndvplptdsranprf 237


RESULT   5
AAB27276
ID   AAB27276 standard; Protein; 310 AA.
XX
AC   AAB27276;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Human confluency regulated adhesion molecule 1 #2.
XX
KW   Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW   inflammation; cancer; wound; angiogenesis; human;
KW   confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS   Homo sapiens.
XX
PN   WO200053749-A2.
XX
PD   14-SEP-2000.
XX
PF   13-MAR-2000; 2000WO-EP02219.
XX
PR   11-MAR-1999;   99EP-0200746.
XX
PA   (RMFD-) RMF DICTAGENE SA.
XX
PI   Imhof BA,  Aurrand-Lions M;
XX
DR   WPI; 2000-587436/55.
DR   N-PSDB; AAA95306.
XX
PT   Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT   CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT   reactions and modulating vascular permeability -
XX
PS   Claim 2; Fig 6; 59pp; English.
XX
CC   The present sequence is the human confluency regulated adhesion molecule
CC   1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC   proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC   and coding sequence can be used in the treatment of cancer, inflammation,
CC   to modulate cell-cell interactions and angiogenesis, and in the
CC   modulation of wound healing.
XX
     Sequence   310 AA;


  Query Match             7.7%;  Score 24;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    167 PRPHYSWYRNDVPLPTDSRANPRF 190
          ||||||||||||||||||||||||
Db    167 prphyswyrndvplptdsranprf 190


RESULT   6
AAB33457
ID   AAB33457 standard; Protein; 310 AA.
XX
AC   AAB33457;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58622.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 88; 309pp; English.
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```
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   310 AA;

  Query Match             7.7%;  Score 24;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 PRPHYSWYRNDVPLPTDSRANPRF 190
           ||||||||||||||||||||||||
Db     167 prphyswyrndvplptdsranprf 190


RESULT   7
AAY96735
ID   AAY96735 standard; Protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
     Key             Location/Qualifiers
     Peptide         1..30
                     /label= Signal_peptide
FT   Modified-site   26..31
FT                   /note= "N-myristoylation site"
FT   Modified-site   69..77
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   104..107
FT                   /note= "N-glycosylation site"
FT   Modified-site   106..109
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   107..110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                        phosphorylation site"
FT   Modified-site   192..195
FT                   /note= "N-glycosylation site"
FT   Modified-site   215..220
FT                   /note= "N-myristoylation site"
FT   Modified-site   226..231
FT                   /note= "N-myristoylation site"
FT   Domain          243..263
FT                   /label= Transmembrane_domain
FT   Modified-site   243..248
FT                   /note= "N-myristoylation site"
FT   Modified-site   244..249
FT                   /note= "N-myristoylation site"
FT   Modified-site   262..267
FT                   /note= "N-myristoylation site"
FT   Modified-site   296..299
FT                   /note= "Casein kinase II phosphorylation site"
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US28634.
XX
PR   16-DEC-1998;   98US-0112851.
PR   16-DEC-1998;   98US-0113145.
PR   22-DEC-1998;   98US-0113511.
PR   12-JAN-1999;   99US-0115558.
PR   12-JAN-1999;   99US-0115565.
PR   12-JAN-1999;   99US-0115733.
PR   09-FEB-1999;   99US-0119341.
PR   10-FEB-1999;   99US-0119537.
PR   12-FEB-1999;   99US-0119965.
PR   02-JUN-1999;   99WO-US12252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51265.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide
XX
PS   Claim 1; Fig 14; 154pp; English.
XX
CC   This is PRO1868, a putative homologue of A33 antigen, a known
CC   colorectal cancer-associated marker. The invention concerns novel
CC   secreted and transmembrane proteins, designated PRO polypeptides. The
CC   cDNA and gene sequences are useful in the recombinant production of PRO
CC   polypeptides, as a hybridization probe to screen libraries to isolate
CC   cDNAs with sequence identity to PRO polypeptides or to map the gene
CC   encoding the PRO polypeptides and analyzing genetic disorders. The
CC   cDNA/gene can also be used to produce transgenic animals useful for the
CC   development and screening of therapeutically useful reagents. They can
CC   also be used in gene therapy, e.g. to replace a defective gene.
XX
SQ   Sequence   310 AA;

  Query Match             7.7%;  Score 24;  DB 21;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 PRPHYSWYRNDVPLPTDSRANPRF 190
           ||||||||||||||||||||||||
Db     167 prphyswyrndvplptdsranprf 190


RESULT   8
AAY96294
ID   AAY96294 standard; protein; 310 AA.
XX
AC   AAY96294;
XX
DT   16-AUG-2000  (first entry)
XX
DE   Human IGFAM-6 immunoglobulin.
XX
KW   Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
KW   infection; inflammation; haematopoiesis; AIDS; allergy.
XX
```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= signal_peptide
FT Protein 31..310
FT /label= IGFAM-6
FT Domain 46..117
FT /label= Ig_domain
FT Domain 153..221
FT /label= Ig_domain
FT Domain 238..260
FT /label= transmembrane_domain
XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.
XX
PF 19-NOV-1999; 99WO-US27566.
XX
PR 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lal P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27386.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT -
XX
PS Claim 1; Page 82-83; 105pp; English.
XX
CC The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-6. Its gene was isolated from a cDNA library of leg
CC tissue. It is expressed in reproductive, nervous and
CC cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 21; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 9
AAM93323
ID AAM93323 standard; Protein; 310 AA.
XX
AC AAM93323;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 2845.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94243.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 2845; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 10
AAM93905
ID AAM93905 standard; Protein; 310 AA.
XX
AC AAM93905;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 4051.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX

PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94867.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 4051; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 11
AAU12440
ID AAU12440 standard; Protein; 310 AA.
XX
AAU12440;

24-OCT-2001 (first entry)
XX
DE Human PRO1868 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21512.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical -
XX
PS Claim 12; Fig 538; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 12
AAB80272

ID AAB80272 standard; Protein; 310 AA.
XX
AC AAB80272;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO1868 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR N-PSDB; AAF72433.

Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
XX
PS Claim 1; Fig 124; 393pp; English.
XX
CC The present sequence is one of sixty one novel secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosum.
CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 13
AAB80383
ID AAB80383 standard; protein; 310 AA.
XX
AC AAB80383;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #13.
XX
KW Secreted protein; human; autoimmune; hyperproliferation;
KW cardiovascular; cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US19735.
XX
PR 23-JUL-1999; 99US-0145220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections -
XX
PS Claim 11; Page 538-539; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 14
AAB80408
ID AAB80408 standard; protein; 310 AA.
XX
AC AAB80408;
XX
DT 24-APR-2001 (first entry)

XX
DE Secreted protein encoded by gene #38.
XX
KW Secreted protein; human; autoimmune; hyperproliferation;
KW cardiovascular; cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US19735.
XX
PR 23-JUL-1999; 99US-0145220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections -
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 15
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation;
KW cardiovascular; cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US19735.
XX
PR 23-JUL-1999; 99US-0145220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections -
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ Sequence 310 AA;

Query Match 7.7%; Score 24; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 16
AAB38333
ID AAB38333 standard; Protein; 311 AA.
XX
AC AAB38333;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW vulnerary; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200061623-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08979.
XX
PR 09-APR-1999; 99US-0128693.
PR 26-APR-1999; 99US-0130991.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;
XX
DR WPI; 2000-647418/62.
XX
PT New nucleic acid molecules encoding 62 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -

XX
PS Claim 11; Page 603-604; 716pp; English.
XX
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.
XX
SQ Sequence 311 AA;

Query Match 7.7%; Score 24; DB 21; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 17
AAB38383
ID AAB38383 standard; Protein; 311 AA.
XX
AC AAB38383;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW vulnerary; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200061623-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08979.
XX
PR 09-APR-1999; 99US-0128693.
PR 26-APR-1999; 99US-0130991.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;
XX
DR WPI; 2000-647418/62.
XX
PT New nucleic acid molecules encoding 62 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 11; Page 642-643; 716pp; English.
XX
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.
XX
SQ Sequence 311 AA;

Query Match 7.7%; Score 24; DB 21; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 18
AAB38384
ID AAB38384 standard; Protein; 311 AA.
XX
AC AAB38384;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 13 clone HAPSA79.
XX
KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; opthalmalogical; human;
KW vulnerary; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200061623-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US08979.
XX
PR 09-APR-1999; 99US-0128693.
PR 26-APR-1999; 99US-0130991.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;
XX
DR WPI; 2000-647418/62.
XX
PT New nucleic acid molecules encoding 62 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 11; Page 643-644; 716pp; English.
XX
CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical

CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.
XX
SQ Sequence 311 AA;

Query Match 7.7%; Score 24; DB 21; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 167 prphyswyrndvplptdsranprf 190

RESULT 19
AAB80431
ID AAB80431 standard; peptide; 339 AA.
XX
AC AAB80431;
XX
DT 24-APR-2001 (first entry)
XX
DE Gene #13 associated peptide #1.
XX
KW Secreted protein; human; autoimmune; hyperproliferation;
KW cardiovascular; cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US19735.
XX
23-JUL-1999; 99US-0145220.
(HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for
PT diagnosing, preventing and treating e.g. autoimmune,
PT hyperproliferative, cardiovascular, and ocular diseases or disorders
PT and microorganism infections -
XX
PS Disclosure; Page 75; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections
CC caused by bacteria, viruses and fungi and ocular disorders e.g.
CC corneal infection. Also used in food preparations.
XX
SQ Sequence 339 AA;

Query Match 7.7%; Score 24; DB 22; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 PRPHYSWYRNDVPLPTDSRANPRF 190
||||||||||||||||||||||||
Db 196 prphyswyrndvplptdsranprf 219

RESULT 20
ABG12109
ID ABG12109 standard; Protein; 404 AA.
XX
AC ABG12109;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12100.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS76296.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 42468; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 404 AA;

```
  Query Match             7.7%;  Score 24;  DB 22;  Length 404;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    167 PRPHYSWYRNDVPLPTDSRANPRF 190
          ||||||||||||||||||||||||
Db    214 prphyswyrndvplptdsranprf 237


RESULT  21
ABG22401
ID   ABG22401 standard; Protein; 361 AA.
XX
AC   ABG22401;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #22392.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS86588.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
     Claim 20; SEQ ID No 52760; 103pp; English.

     The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   361 AA;
```

```
  Query Match             6.8%;  Score 21;  DB 22;  Length 361;
  Best Local Similarity   100.0%;  Pred. No. 1e-11;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    170 HYSWYRNDVPLPTDSRANPRF 190
          |||||||||||||||||||||
Db    179 hyswyrndvplptdsranprf 199


RESULT  22
ABG22398
ID   ABG22398 standard; Protein; 68 AA.
XX
AC   ABG22398;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #22389.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS86585.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 52757; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;
```

```
  Query Match             4.8%;  Score 15;  DB 22;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      58 SQTSDPRIEWKKIQD 72
           |||||||||||||||
Db      37 sqtsdpriewkkiqd 51


RESULT  23
AAY11472
ID   AAY11472 standard; Protein; 89 AA.
XX
AC   AAY11472;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human 5' EST secreted protein SEQ ID No 294.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
     forensic; gene therapy; chromosome mapping; signal peptide;
     upstream regulatory sequence; cytokine activity; cell proliferation;
     differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS   Homo sapiens.
XX
PN   WO9906551-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01235.
XX
PR   01-AUG-1997;   97US-0905133.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153781/13.
DR   N-PSDB; AAX39538.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 34; Page 394; 434pp; English.

     AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
     human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence   89 AA;


  Query Match             4.8%;  Score 15;  DB 20;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      58 SQTSDPRIEWKKIQD 72
           |||||||||||||||
Db      58 sqtsdpriewkkiqd 72


RESULT  24
ABG27038
ID   ABG27038 standard; Protein; 267 AA.
XX
AC   ABG27038;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #27029.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS91225.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 57397; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   267 AA;


  Query Match             3.2%;  Score 10;  DB 22;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy    244 GIIGGVLVVL 253
          ||||||||||
Db    135 giiggvlvvl 144


RESULT  25
AAW01191
ID   AAW01191 standard; Peptide; 48 AA.
XX
AC   AAW01191;
XX
DT   15-MAR-1997  (first entry)
XX
DE   Serine protease PfSP12-52 N-terminal fragment.
XX
KW   Flea; midgut; serine protease; PfSP12-52; vaccine;
KW   domestic animal; infestation; insecticide; protease-inhibitor;
KW   controlled release formulation; synergist.
XX
OS   Siphonaptera sp.

FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "Signal peptide"
FT   Peptide         20..48
FT                   /note= "Part of N-terminal fragment AAW01177"
XX
PN   WO9611706-A1.
XX
PD   25-APR-1996.
XX
PF   18-OCT-1995;   95WO-US14442.
XX
PR   07-JUN-1995;   95US-0485455.
PR   18-OCT-1994;   94US-0326773.
PR   07-JUN-1995;   95US-0482130.
PR   07-JUN-1995;   95US-0484211.
PR   07-JUN-1995;   95US-0485443.
XX
PA   (PARA-) PARAVAX INC.
PA   (HESK-) HESKA CORP.
XX
PI   Arfsten A,  Dale B,  Frank GR,  Grieve RB,  Heath A;
PI   Hunter SW,  Rushlow KE, Stiegler GL,  Yamanaka M;
XX
DR   WPI; 1996-221762/22.
DR   N-PSDB; AAT40836.
XX
PT   DNA encoding Flea serine protease and aminopeptidase - useful in
PT   vaccines to protect animals from flea infestation.
XX
PS   Claim 71; Page 163; 241pp; English.
XX
CC   This sequence represents a partial N-terminal sequence of flea
CC   midgut serine protease, Sp12-52, isolated from a flea cDNA
CC   library by homology with conserved serine protease sequences.
CC   The sequence contains part of N-terminal sequence AAW01177, and other
CC   SP12 sequences are given in AAW01197 (C-terminal sequence) and
CC   AAW01209 (PfSP12-69).  The peptide may be used in a vaccine for
CC   protection of domestic animals from flea infestation, or in
CC   isolation of protease-inhibitors, which may be used in controlled
CC   release formulations to reduce the flea burden on and around the
CC   animal.  The inhibitors may be included in insecticidal
CC   compositions to increase efficacy of other active agents, by
CC   reducing proteolytic activity in the flea midgut.
XX
SQ   Sequence   48 AA;


  Query Match             2.6%;  Score 8;  DB 17;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    252 VLIVLAVI 259
          ||||||||
Db      1 vlivlavi 8


RESULT  26
AAB50588
ID   AAB50588 standard; Protein; 48 AA.
XX
AC   AAB50588;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Flea serine protease nfSP12 N-terminal protein sequence #65.
XX
KW   Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
KW   flea infestation; proteolytic; insecticide; vaccine; cat; dog; dog flea;
KW   Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
KW   ectoparasite.
XX
OS   Ctenocephalides felis.
XX
PN   US6150125-A.
XX
PD   21-NOV-2000.
XX
PF   24-APR-1996;   96US-0639075.
XX
PR   13-DEC-1991;   91US-0806482.
PR   18-OCT-1994;   94US-0326773.
PR   07-JUN-1995;   95US-0482130.
PR   07-JUN-1995;   95US-0484211.
PR   07-JUN-1995;   95US-0485443.
PR   07-JUN-1995;   95US-0485455.
PR   15-AUG-1997;   97WO-US14442.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Gaines PJ,  Silver G,  Rushlow KE,  Hunter SW,  Frank GR,  Stiegler GL;
PI   Grieve RB;
XX
DR   WPI; 2001-136374/14.
DR   N-PSDB; AAC90844.
XX
PT   New isolated flea proteins with proteolytic activity, useful for
PT   preventing and reducing flea infestations in mammals especially cats
PT   and dogs -
XX
PS   Claim 1; Column 47-48; 150pp; English.
XX
CC   The present invention describes isolated flea serine protease,
CC   aminopeptidase and cysteine protease proteins (I). Also described is a
CC   method for identifying a compound (II) capable of inhibiting flea
CC   protease activity comprising: (a) contacting (I) with a protease
CC   substrate and a putative inhibitory compound, where (I) has proteolytic
CC   activity in the absence of the compound; and (b) determining if the
CC   compound inhibits protease activity by detecting cleavage of the
CC   protease substrates; where decreased cleavage of the protease substrate
CC   indicates an inhibitory compound. (I), nucleic acid molecules encoding
CC   (I), and antibodies immunospecific for (I) and (II) are useful for
CC   preventing and reducing flea infestations, particularly the species
CC   Ctenocephalides felis (cat fleas), Ctenocephalides canis (dog fleas) and
CC   Pulex irritans, in animals, preferably cats and dogs. They are also
CC   useful for reducing infestation by other ectoparasites, preferably
CC   mosquitoes, midges, sandflies, blackflies, ticks and Rhodnius. AAC90818
CC   to AAC90913 and AAB50551 to AAB50644 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   48 AA;


  Query Match             2.6%;  Score 8;  DB 22;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 5;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    252 VLIVLAVI 259
          ||||||||
Db      1 vlivlavi 8
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RESULT 27
AAG81659
ID AAG81659 standard; Protein; 204 AA.
XX
AC AAG81659;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame protein sequence SEQ ID NO:412.
XX
KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;
KW vaccination; endocarditis.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
DR N-PSDB; AAH52509.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 18; Page 151; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 204 AA;

Query Match 2.6%; Score 8; DB 22; Length 204;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    242 IAGIIGGV 249
          ||||||||
Db    181 iagiiggv 188
```

RESULT 28
AAG82062
ID AAG82062 standard; Protein; 204 AA.
XX
AC AAG82062;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame protein sequence SEQ ID NO:1218.
XX
KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;
KW vaccination; endocarditis.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
DR N-PSDB; AAH52912.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 18; Page 349; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 204 AA;

Query Match 2.6%; Score 8; DB 22; Length 204;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    242 IAGIIGGV 249
          ||||||||
Db    181 iagiiggv 188
```

RESULT 29
AAW41974
ID AAW41974 standard; Protein; 246 AA.

XX
AC AAW41974;
XX
DT 02-JUL-1998 (first entry)
XX
DE Flea serine protease SEQ ID NO:129.
XX
KW Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;
KW immunoglobulin protease; larvae; host animal.
XX
OS Siphonaptera.
XX
FH Key Location/Qualifiers
FT Misc-difference 241
FT /note= "encoded by TAA, a stop codon"
XX
PN WO9740058-A1.
XX
PD 30-OCT-1997.
XX
PF 24-APR-1997; 97WO-US06121.
XX
PR 04-APR-1997; 97US-0042945.
PR 24-APR-1996; 96US-0639075.
PR 15-NOV-1996; 96US-0749699.
XX
PA (HESK-) HESKA CORP.
XX
PI Frank GR, Gaines PJ, Grieve RB, Hunter SW, Rushlow KE;
PI Silver G, Stiegler GL;
XX
DR WPI; 1998-076762/07.
DR N-PSDB; AAV04597.
XX
PT New flea protease genes and proteins - used in vaccine compositions
PT for the prophylaxis and treatment of flea infestation, especially in
PT cats or dogs
XX
PS Claim 2; Page 260-261; 318pp; English.
XX
CC The present sequence represents a novel flea serine protease. The
CC protease, its mimetopes, antibodies (Ab) and inhibitors of the
CC protein, as well as the DNA encoding the protein, may all be used in
CC therapeutic compositions to reduce flea protease activity (especially
CC immunoglobulin protease) and so reduce flea infestation, especially in
CC cats or dogs. Alternatively, flea larvae may ingest the faeces of adult
CC fleas which comprises anti-protease antibodies produced by a host animal
in response to administration of the protein. Therapeutic compositions
may further comprise a compound that reduces haematophagous ectoparasite
burden by a method other than by reducing flea immunoglobulin protease
CC activity. The novel flea DNA encoding the protein can also used to
CC produce recombinant protein, and fragments of it are used as probes and
CC primers for identification and isolation of related sequences, also as
CC antisense, triplex-forming agents and ribozymes for inhibition of the
CC synthesis of the protein. Ab are also useful for screening expression
CC libraries, to purify the protein and to target cytotoxins to fleas.
XX
SQ Sequence 246 AA;

Query Match 2.6%; Score 8; DB 19; Length 246;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
||||||||
Db 2 vlivlavi 9

RESULT 30
AAB50616
ID AAB50616 standard; Protein; 246 AA.
XX

AC AAB50616;
XX
DT 19-MAR-2001 (first entry)
XX
DE Flea serine protease PfSP12-246 protein sequence #127.
XX
KW Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; dog flea;
KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
KW ectoparasite.
XX
OS Ctenocephalides felis.
XX
PN US6150125-A.
XX
PD 21-NOV-2000.
XX
PF 24-APR-1996; 96US-0639075.
XX
PR 13-DEC-1991; 91US-0806482.
PR 18-OCT-1994; 94US-0326773.
PR 07-JUN-1995; 95US-0482130.
PR 07-JUN-1995; 95US-0484211.
PR 07-JUN-1995; 95US-0485443.
PR 07-JUN-1995; 95US-0485455.
PR 15-AUG-1997; 97WO-US14442.
XX
PA (HESK-) HESKA CORP.
XX
PI Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR, Stiegler GL;
PI Grieve RB;
XX
DR WPI; 2001-136374/14.
DR N-PSDB; AAC90878.
XX
PT New isolated flea proteins with proteolytic activity, useful for
PT preventing and reducing flea infestations in mammals especially cats
PT and dogs -
XX
PS Claim 1; Column 195-198; 150pp; English.
XX
CC The present invention describes isolated flea serine protease,
CC aminopeptidase and cysteine protease proteins (I). Also described is a
CC method for identifying a compound (II) capable of inhibiting flea
CC protease activity comprising: (a) contacting (I) with a protease
CC substrate and a putative inhibitory compound, where (I) has proteolytic
CC activity in the absence of the compound; and (b) determining if the
CC compound inhibits protease activity by detecting cleavage of the
CC protease substrates; where decreased cleavage of the protease substrate
CC indicates an inhibitory compound. (I), nucleic acid molecules encoding
CC (I), and antibodies immunospecific for (I) and (II) are useful for
CC preventing and reducing flea infestations, particularly the species
CC Ctenocephalides felis (cat fleas), Ctenocephalides canis (dog fleas) and
CC Pulex irritans, in animals, preferably cats and dogs. They are also
CC useful for reducing infestation by other ectoparasites, preferably
CC mosquitoes, midges, sandflies, blackflies, ticks and Rhodnius. AAC90818
CC to AAC90913 and AAB50551 to AAB50644 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 246 AA;

Query Match 2.6%; Score 8; DB 22; Length 246;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 VLIVLAVI 259
||||||||
Db 2 vlivlavi 9

RESULT 31
AAG93112

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:32:47 ; Search time 23.64 Seconds
(without alignments)
320.302 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

d size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	48	1	US-08-485-455D-65	Sequence 65, Appl
2	8	2.6	48	2	US-08-482-130C-65	Sequence 65, Appl
3	8	2.6	48	2	US-08-484-211C-65	Sequence 65, Appl
4	8	2.6	48	3	US-08-906-769-65	Sequence 65, Appl
5	8	2.6	48	3	US-08-906-616-65	Sequence 65, Appl
6	8	2.6	48	4	US-08-817-795-65	Sequence 65, Appl
7	8	2.6	48	4	US-08-485-443B-65	Sequence 65, Appl
8	8	2.6	48	4	US-08-639-075A-65	Sequence 65, Appl
9	8	2.6	48	4	US-09-012-431-65	Sequence 65, Appl
10	8	2.6	48	4	US-09-012-692-65	Sequence 65, Appl
11	8	2.6	48	4	US-08-906-613-65	Sequence 65, Appl
12	8	2.6	48	5	PCT-US95-14442A-65	Sequence 65, Appl
13	8	2.6	246	3	US-08-906-769-127	Sequence 127, App
14	8	2.6	246	3	US-08-906-616-127	Sequence 127, App
15	8	2.6	246	4	US-08-639-075A-127	Sequence 127, App
16	8	2.6	246	4	US-09-012-431-127	Sequence 127, App
17	8	2.6	246	4	US-09-012-692-127	Sequence 127, App
18	8	2.6	246	4	US-08-906-613-127	Sequence 127, App
19	7	2.3	170	3	US-09-189-035-2	Sequence 2, Appli
20	7	2.3	170	4	US-09-382-086-2	Sequence 2, Appli
21	7	2.3	249	2	US-09-154-802-1	Sequence 1, Appli
22	7	2.3	249	3	US-09-373-029-1	Sequence 1, Appli
23	7	2.3	758	4	US-09-413-814-32	Sequence 32, Appl
24	7	2.3	775	1	US-07-603-133B-15	Sequence 15, Appl
25	7	2.3	775	1	US-07-603-133B-16	Sequence 16, Appl
26	7	2.3	1186	2	US-08-861-464-8	Sequence 8, Appli
27	7	2.3	1186	2	US-08-396-001-8	Sequence 8, Appli
28	7	2.3	1186	4	US-09-323-433A-8	Sequence 8, Appli
29	7	2.3	1395	4	US-09-540-245A-15	Sequence 15, Appl
30	6	1.9	14	2	US-08-685-589A-164	Sequence 164, App
31	6	1.9	27	4	US-09-227-357-276	Sequence 276, App
32	6	1.9	29	1	US-07-960-510-4	Sequence 4, Appli
33	6	1.9	29	1	US-07-960-510-5	Sequence 5, Appli
34	6	1.9	29	1	US-07-960-510-6	Sequence 6, Appli
35	6	1.9	29	1	US-07-960-510-7	Sequence 7, Appli
36	6	1.9	35	6	5171673-7	Patent No. 5171673
37	6	1.9	45	3	US-09-053-197A-72	Sequence 72, Appl
38	6	1.9	45	4	US-09-085-761A-77	Sequence 77, Appl
39	6	1.9	48	1	US-07-796-361A-15	Sequence 15, Appl
40	6	1.9	93	1	US-08-591-498-1	Sequence 1, Appli
41	6	1.9	115	2	US-08-672-345C-18	Sequence 18, Appl
42	6	1.9	115	2	US-08-672-345C-108	Sequence 108, App
43	6	1.9	115	4	US-09-214-095D-18	Sequence 18, Appl
44	6	1.9	115	4	US-09-214-095D-98	Sequence 98, Appl
45	6	1.9	123	2	US-08-822-573-2	Sequence 2, Appli
46	6	1.9	132	1	US-08-591-498-16	Sequence 16, Appl
47	6	1.9	145	4	US-09-096-244-2	Sequence 2, Appli
48	6	1.9	158	2	US-08-846-762-2	Sequence 2, Appli
49	6	1.9	208	2	US-08-700-607-7	Sequence 7, Appli
50	6	1.9	219	1	US-08-441-629-13	Sequence 13, Appl
51	6	1.9	219	3	US-08-776-207-13	Sequence 13, Appl
52	6	1.9	219	5	PCT-US95-09172-13	Sequence 13, Appl
53	6	1.9	228	2	US-08-417-495-27	Sequence 27, Appl
54	6	1.9	228	2	US-08-284-391B-27	Sequence 27, Appl
55	6	1.9	228	4	US-09-218-950-27	Sequence 27, Appl
56	6	1.9	228	5	PCT-US92-01785-27	Sequence 27, Appl
57	6	1.9	228	5	PCT-US95-00454-27	Sequence 27, Appl
58	6	1.9	236	3	US-08-705-771-19	Sequence 19, Appl
59	6	1.9	255	3	US-08-906-769-91	Sequence 91, Appl
60	6	1.9	255	3	US-08-906-616-91	Sequence 91, Appl
61	6	1.9	255	4	US-08-817-795-91	Sequence 91, Appl
62	6	1.9	255	4	US-08-639-075A-91	Sequence 91, Appl
63	6	1.9	255	4	US-09-012-431-91	Sequence 91, Appl
64	6	1.9	255	4	US-09-012-692-91	Sequence 91, Appl
65	6	1.9	255	4	US-08-906-613-91	Sequence 91, Appl
66	6	1.9	255	5	PCT-US95-14442A-91	Sequence 91, Appl
67	6	1.9	265	2	US-08-807-044-1	Sequence 1, Appli
68	6	1.9	266	6	5175383-5	Patent No. 5175383
69	6	1.9	267	1	US-08-462-169B-13	Sequence 13, Appl
70	6	1.9	267	2	US-08-700-607-8	Sequence 8, Appli
71	6	1.9	267	3	US-09-103-079-13	Sequence 13, Appl
72	6	1.9	268	1	US-08-439-725A-12	Sequence 12, Appl
73	6	1.9	268	1	US-08-464-590A-17	Sequence 17, Appl
74	6	1.9	268	2	US-08-207-412B-12	Sequence 12, Appl
75	6	1.9	268	2	US-08-867-471-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-485-455D-65
; Sequence 65, Application US/08485455D
; Patent No. 5712143
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary L.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,455D
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-455D-65


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  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     252 VLIVLAVI 259
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Db       1 VLIVLAVI 8


RESULT   2
US-08-482-130C-65
; Sequence 65, Application US/08482130C
; Patent No. 5962257
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary L.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,130C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-482-130C-65


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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     252 VLIVLAVI 259
           ||||||||
Db       1 VLIVLAVI 8


RESULT   3
US-08-484-211C-65
; Sequence 65, Application US/08484211C
; Patent No. 5972645
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary L.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,211C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  48 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-484-211C-65


  Query Match             2.6%;  Score 8;  DB 2;  Length 48;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     252 VLIVLAVI 259
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Db       1 VLIVLAVI 8


RESULT   4
US-08-906-769-65
; Sequence 65, Application US/08906769
; Patent No. 6077687
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:33:22 ; Search time 30.81 Seconds
(without alignments)
966.819 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

d size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	146	2	F70313	hypothetical prote
2	8	2.6	204	2	A89919	conserved hypothet
3	8	2.6	208	2	D83431	type III export pr
4	8	2.6	506	2	T02400	probable beta-gluc
5	8	2.6	959	2	E85276	hypothetical prote
6	7	2.3	118	1	G1YC	gene 1 protein - S
7	7	2.3	128	2	C83448	succinate dehydrog
8	7	2.3	137	2	B41047	exsB protein - Pse
9	7	2.3	137	2	E83433	exoenzyme S synthe
10	7	2.3	173	2	B90241	hypothetical prote
11	7	2.3	177	2	E85833	partial probable s
12	7	2.3	177	2	B90988	partial probable s
13	7	2.3	194	2	T28889	hypothetical prote
14	7	2.3	208	2	T03627	GTP-binding protei
15	7	2.3	208	2	T01588	GTP-binding protei
16	7	2.3	214	2	T47268	phosphatidylserine
17	7	2.3	224	2	D71915	hydrogenase, cytoc
18	7	2.3	232	2	S60984	hypothetical prote
19	7	2.3	246	2	F91238	PTS system, fructo
20	7	2.3	246	2	B86086	PTS system, fructo
21	7	2.3	249	2	G84224	hypothetical prote
22	7	2.3	255	2	B72474	hypothetical prote
23	7	2.3	267	2	B83705	phosphonates trans
24	7	2.3	269	1	C69651	prolipoprotein dia
25	7	2.3	280	2	H83623	probable chemotaxi
26	7	2.3	287	2	E75159	hypothetical prote
27	7	2.3	322	2	E69009	cation antiporter
28	7	2.3	324	2	T27302	hypothetical prote
29	7	2.3	332	1	DEBYG1	glyceraldehyde-3-p
30	7	2.3	332	1	DEBYG2	glyceraldehyde-3-p
31	7	2.3	332	2	C72485	probable high-affi
32	7	2.3	335	2	S29813	glyceraldehyde-3-p
33	7	2.3	337	2	AI2360	hypothetical prote
34	7	2.3	348	2	E84143	L-iditol 2-dehydro
35	7	2.3	359	2	H65201	pts system, fructo
36	7	2.3	380	2	H75159	3-isopropylmalate
37	7	2.3	387	2	E90533	nitrogen fixation
38	7	2.3	402	2	G83367	hypothetical prote
39	7	2.3	421	2	H86217	protein T27G7.16 (
40	7	2.3	422	2	D70110	aminotransferase (
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43	7	2.3	445	2	S75859	hypothetical prote
44	7	2.3	452	2	A70389	seryl-tRNA(Sec) se
45	7	2.3	473	2	T28118	hypothetical prote
46	7	2.3	491	1	O4RBPC	cytochrome P450 2B
47	7	2.3	491	2	S31277	cytochrome P450 2B
48	7	2.3	491	2	S31278	cytochrome P450 2B
49	7	2.3	491	2	S35666	cytochrome P450 2B
50	7	2.3	505	2	C69666	NADH dehydrogenase
51	7	2.3	512	2	B69146	gluthatione-regula
52	7	2.3	544	2	AE3375	methionyl-tRNA syn
53	7	2.3	554	2	S50309	hypothetical prote
54	7	2.3	573	2	AF1418	ABC transporter, A
55	7	2.3	573	2	AH1793	ABC transporter, A
56	7	2.3	578	2	G82950	conserved hypothet
57	7	2.3	586	2	S63386	HOL1 protein - yea
58	7	2.3	667	2	T35491	probable serine/th
59	7	2.3	697	2	S09254	colicin D - Escher
60	7	2.3	703	2	T32572	hypothetical prote
61	7	2.3	758	1	S45477	SEC18 protein - ye
62	7	2.3	774	1	VPXRWT	outer layer protei
63	7	2.3	775	1	VPXRW7	outer layer protei
64	7	2.3	776	1	VPXRW9	outer layer protei
65	7	2.3	782	2	E90427	hypothetical prote
66	7	2.3	805	2	A64453	H+-transporting AT
67	7	2.3	810	2	AF2425	phenylalanyl-tRNA
68	7	2.3	832	2	G97146	probable permease
69	7	2.3	840	2	A27832	cell division cont
70	7	2.3	841	2	T01011	hypothetical prote
71	7	2.3	1105	2	B64973	yegE protein - Esc
72	7	2.3	1213	2	S42368	guanine nucleotide
73	7	2.3	1400	2	A71514	probable protein e
74	7	2.3	1785	2	T21558	hypothetical prote
75	7	2.3	1929	2	T21559	hypothetical prote

ALIGNMENTS

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F70313
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
C;Accession: F70313
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: F70313
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-146 <AQF>
A;Cross-references: GB:AE000675; NID:g2982863; PIDN:AAC06501.1; PID:g2982881; GB:AE00
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_142
C;Superfamily: Aquifex aeolicus hypothetical protein aq_142

Query Match 2.6%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 VLIVLAVI 12

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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89919
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <KUR>
A;Cross-references: GB:BA000018; PID:g13701215; PIDN:BAB42510.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1250

Query Match 2.6%; Score 8; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IAGIIGGV 249
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Db 181 IAGIIGGV 188

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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83431
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
an, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
ory, S.; Olson, M.V.
re 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337
A;Accession: D83431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05113.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: pscK; PA1724

Query Match 2.6%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRRLRLRL 11
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Db 160 SRRLRLRL 167

RESULT 4
T02400
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02400; F84878
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
A;Reference number: Z14667
A;Accession: T02400
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-506 <ROU>
A;Cross-references: EMBL:AC004521; NID:g3128166; PIDN:AAC16091.1; PID:g3128187
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <STO>
A;Cross-references: GB:AE002093; NID:g3128187; PIDN:AAC16091.1; GSPDB:GN00139
C;Genetics:
A;Gene: F4I1.26; At2g44450
A;Map position: 2
A;Introns: 50/3; 74/1; 93/3; 119/1; 145/1; 174/2; 259/3; 370/1; 380/3; 415/1; 447/2
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 2.6%; Score 8; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLIVLA 257
||||||||
Db 9 LVVLIVLA 16

RESULT 5
E85276
hypothetical protein AT4g24020 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: E85276
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: E85276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-959 <STO>
A;Cross-references: GB:NC_001268; NID:g7269251; PIDN:CAB81320.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g24020
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

Query Match 2.6%; Score 8; DB 2; Length 959;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 EAVNLKSS 37
||||||||
Db 300 EAVNLKSS 307

RESULT 6
G1YC

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:39:47 ; Search time 17.64 Seconds
(without alignments)
680.446 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

[redacted] size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	146	1	Y142_AQUAE	O66537 aquifex aeo
2	7	2.3	118	1	ATPZ_SYNP6	P08443 synechococc
3	7	2.3	137	1	EXSB_PSEAE	P26994 pseudomonas
4	7	2.3	224	1	XLR1_MOUSE	Q9z114 mus musculu
5	7	2.3	232	1	YOZ1_YEAST	Q99210 saccharomyc
6	7	2.3	269	1	LGT_BACSU	O34752 bacillus su
7	7	2.3	280	1	CHR2_PSEAE	Q9i6v7 pseudomonas
8	7	2.3	331	1	G3P2_YEAST	P00358 saccharomyc
9	7	2.3	331	1	G3P3_YEAST	P00359 saccharomyc
10	7	2.3	335	1	G3P1_TRIKO	P17729 trichoderma
11	7	2.3	359	1	PTWC_ECOLI	P32672 escherichia
12	7	2.3	374	1	RL4_TRYBB	P49669 trypanosoma
13	7	2.3	422	1	CSD_BORBU	O51111 borrelia bu
14	7	2.3	452	1	SELA_AQUAE	O67140 aquifex aeo
15	7	2.3	473	1	YS81_CAEEL	Q09621 caenorhabdi
16	7	2.3	491	1	CPB4_RABIT	P00178 oryctolagus
17	7	2.3	491	1	CPB5_RABIT	P12789 oryctolagus
18	7	2.3	501	1	C6AH_DROME	Q9v770 drosophila
19	7	2.3	502	1	C6AN_DROME	Q9v771 drosophila
20	7	2.3	505	1	NDHF_BACSU	P39755 bacillus su
21	7	2.3	586	1	HOL1_YEAST	P53389 saccharomyc
22	7	2.3	697	1	CEAD_ECOLI	P17998 escherichia
23	7	2.3	758	1	SC18_YEAST	P18759 saccharomyc
24	7	2.3	774	1	VP4_ROTHT	P11200 human rotav
25	7	2.3	775	1	VP4_ROTHM	P11197 human rotav
26	7	2.3	776	1	VP4_ROTHN	P11199 human rotav
27	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
28	7	2.3	1015	1	YA17_HUMAN	Q9upz3 homo sapien
29	7	2.3	1105	1	YEGE_ECOLI	P38097 escherichia
30	7	2.3	1234	1	YNX5_CAEEL	P34578 caenorhabdi
31	7	2.3	2871	1	FBN1_BOVIN	P98133 bos taurus
32	7	2.3	2871	1	FBN1_HUMAN	P35555 homo sapien
33	7	2.3	2871	1	FBN1_MOUSE	Q61554 mus musculu
34	7	2.3	2871	1	FBN1_PIG	Q9tv36 sus scrofa
35	6	1.9	39	1	PSBJ_ODOSI	P49512 odontella s
36	6	1.9	56	1	SCP2_MESMA	Q9njp7 mesobuthus
37	6	1.9	56	1	SCP3_MESMA	Q9u8d1 mesobuthus
38	6	1.9	64	1	YDT6_SCHPO	O14211 schizosacch
39	6	1.9	74	1	SRP_SOYBN	Q07502 glycine max
40	6	1.9	86	1	PTHP_STRMU	P45596 streptococc
41	6	1.9	87	1	PTHP_BACHD	Q9k8d2 bacillus ha
42	6	1.9	87	1	PTHP_STRBO	Q9wxk8 streptococc
43	6	1.9	87	1	PTHP_STRSL	P24366 streptococc
44	6	1.9	87	1	Y14B_BPT4	P32280 bacteriopha
45	6	1.9	89	1	IAPP_FELCA	P12967 felis silve
46	6	1.9	94	1	YE23_HAEIN	P44194 haemophilus
47	6	1.9	102	1	KCRB_PIG	Q29594 sus scrofa
48	6	1.9	105	1	SP12_CAEEL	O44953 caenorhabdi
49	6	1.9	113	1	RL31_SCHPO	Q9urx6 schizosacch
50	6	1.9	118	1	YKD7_YEAST	P32858 saccharomyc
51	6	1.9	120	1	GALP_PIG	Q9tt95 sus scrofa
52	6	1.9	126	1	PFDB_SULSO	Q9uxb8 sulfolobus
53	6	1.9	126	1	SECE_VIBAL	Q9zne7 vibrio algi
54	6	1.9	126	1	SECE_VIBCH	Q9kv36 vibrio chol
55	6	1.9	127	1	Y080_METJA	Q60386 methanococc
56	6	1.9	130	1	KV5G_MOUSE	P01639 mus musculu
57	6	1.9	130	1	Y06O_BPT4	P39222 bacteriopha
58	6	1.9	130	1	YFFQ_ECOLI	P76548 escherichia
59	6	1.9	132	1	AMP1_ALLCE	Q41258 allium cepa
60	6	1.9	134	1	YFID_BACSU	P54720 bacillus su
61	6	1.9	137	1	Y541_ARCFU	O29709 archaeoglob
62	6	1.9	138	1	NIKR_ARCFU	O29515 archaeoglob
63	6	1.9	143	1	CU17_BOMMO	O02387 bombyx mori
64	6	1.9	146	1	RL13_MYCGE	P47657 mycoplasma
65	6	1.9	148	1	PFD2_ARATH	Q9ljg8 arabidopsis
66	6	1.9	152	1	NIRD_PSEST	Q52522 pseudomonas
67	6	1.9	155	1	Y060_BORBU	O51087 borrelia bu
68	6	1.9	157	1	MENG_MYCLE	Q9cdd2 mycobacteri
69	6	1.9	160	1	PETD_CHLEU	P11093 chlamydomon
70	6	1.9	160	1	PETD_GUITH	O78415 guillardia
71	6	1.9	160	1	TATB_HELPJ	Q9zm58 helicobacte
72	6	1.9	161	1	ISPF_BUCAI	P57494 buchnera ap
73	6	1.9	164	1	RL21_ARATH	Q43291 arabidopsis
74	6	1.9	167	1	ILVH_MYCAV	Q59499 mycobacteri
75	6	1.9	167	1	OB_CANFA	O02720 canis famil

ALIGNMENTS

RESULT 1
Y142_AQUAE
ID Y142_AQUAE STANDARD; PRT; 146 AA.
AC O66537;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_142.
GN AQ_142.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC ----------

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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   ---------------------------------------------------------------------------
DR   EMBL; AE000675; AAC06501.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   146 AA;  16321 MW;  9E98228A820CC2B2 CRC64;


  Query Match             2.6%;  Score 8;  DB 1;  Length 146;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    252 VLIVLAVI 259
          ||||||||
Db      5 VLIVLAVI 12


RESULT   2
ATPZ_SYNP6
ID   ATPZ_SYNP6     STANDARD;      PRT;   118 AA.
AC   P08443;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP synthase protein I.
GN   ATPI.
OS   Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=1139;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87311713; PubMed=3041005;
RA   Cozens A.L., Walker J.E.;
RT   "The organization and sequence of the genes for ATP synthase subunits
RT   in the cyanobacterium Synechococcus 6301. Support for an
RT   endosymbiotic origin of chloroplasts.";
RL   J. Mol. Biol. 194:359-383(1987).
CC   -!- FUNCTION: A POSSIBLE FUNCTION FOR THIS PROTEIN IS TO GUIDE THE
CC       ASSEMBLY OF THE MEMBRANE SECTOR OF THE ATPASE ENZYME COMPLEX.
CC   -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
CC   ---------------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X05302; CAA28922.1; -.
DR   PIR; S10825; G1YC.
KW   Hydrogen ion transport; CF(0); Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     73     93       POTENTIAL.
FT   TRANSMEM     94    114       POTENTIAL.
SQ   SEQUENCE   118 AA;  13455 MW;  16B76A47F76CC196 CRC64;


  Query Match             2.3%;  Score 7;  DB 1;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    251 VVLIVLA 257
          |||||||
Db     75 VVLIVLA 81


RESULT   3
EXSB_PSEAE
ID   EXSB_PSEAE     STANDARD;      PRT;   137 AA.
AC   P26994;
DT   01-AUG-1992 (Rel. 23, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Exoenzyme S synthesis protein B.
GN   EXSB OR PA1712.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=92011420; PubMed=1655713;
RA   Frank D.W., Iglewski B.H.;
RT   "Cloning and sequence analysis of a trans-regulatory locus required
RT   for exoenzyme S synthesis in Pseudomonas aeruginosa.";
RL   J. Bacteriol. 173:6460-6468(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
CC   -!- SIMILARITY: TO Y.ENTEROCOLITICA VIRB.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M64975; AAA25815.1; -.
DR   EMBL; AE004597; AAG05101.1; -.
DR   PIR; B41047; B41047.
KW   Complete proteome.
FT   CONFLICT     62     62       R -> W (IN REF. 1).
SQ   SEQUENCE   137 AA;  14996 MW;  F7367E7AB301C4EA CRC64;


  Query Match             2.3%;  Score 7;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 LRLRLYA 13
          |||||||
Db     41 LRLRLYA 47


RESULT   4
XLR1_MOUSE
ID   XLR1_MOUSE     STANDARD;      PRT;   224 AA.
AC   Q9Z1L4;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   X-linked juvenile retinoschisis protein precursor.
GN   RS1 OR RS1H OR XLRS1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:38:12 ; Search time 48.09 Seconds
(without alignments)
1115.168 Million cell updates/sec

Title: US-09-524-531C-13
Perfect score: 310
Sequence: 1 MALSRRLRLRLYARLPHFFL.....VNYIRTSEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	253	81.6	310	11	Q9EPK4	Q9epk4 mus musculu
2	245	79.0	310	11	Q9D1M9	Q9d1m9 mus musculu
3	152	49.0	310	11	Q9D8B7	Q9d8b7 mus musculu
4	24	7.7	309	4	Q96FL1	Q96fl1 homo sapien
5	24	7.7	310	4	Q9BX67	Q9bx67 homo sapien
6	8	2.6	204	16	Q99U70	Q99u70 staphylococ
7	8	2.6	206	2	P95439	P95439 pseudomonas
8	8	2.6	208	16	Q9I313	Q9i313 pseudomonas
9	8	2.6	246	5	Q9XY46	Q9xy46 ctenocephal
10	8	2.6	400	10	Q9LT44	Q9lt44 arabidopsis
11	8	2.6	506	10	O64879	O64879 arabidopsis
12	8	2.6	959	10	O22987	O22987 arabidopsis
13	7	2.3	85	12	Q99GX8	Q99gx8 heliocoverp
14	7	2.3	95	10	Q9FE08	Q9fe08 perilla fru
15	7	2.3	121	2	Q93HQ4	Q93hq4 streptococc
16	7	2.3	125	11	Q9CS62	Q9cs62 mus musculu
17	7	2.3	128	16	Q9I3D7	Q9i3d7 pseudomonas
18	7	2.3	147	5	Q9VZG1	Q9vzg1 drosophila
19	7	2.3	173	17	Q97ZK3	Q97zk3 sulfolobus
20	7	2.3	177	16	Q931Y0	Q931y0 staphylococ
21	7	2.3	194	5	Q22478	Q22478 caenorhabdi
22	7	2.3	208	10	O80501	O80501 arabidopsis
23	7	2.3	208	10	Q40525	Q40525 nicotiana t
24	7	2.3	214	2	O32618	O32618 helicobacte
25	7	2.3	220	11	Q9EQG0	Q9eqg0 mus musculu
26	7	2.3	224	11	Q9R1M6	Q9r1m6 mus musculu
27	7	2.3	224	16	Q9ZLK3	Q9zlk3 helicobacte
28	7	2.3	232	3	Q99210	Q99210 saccharomyc
29	7	2.3	242	17	Q96XA1	Q96xa1 sulfolobus
30	7	2.3	247	4	O75192	O75192 homo sapien
31	7	2.3	249	17	Q9HRJ5	Q9hrj5 halobacteri
32	7	2.3	255	17	Q9Y950	Q9y950 aeropyrum p
33	7	2.3	255	17	Q970E4	Q970e4 sulfolobus
34	7	2.3	267	16	Q9KFN7	Q9kfn7 bacillus ha
35	7	2.3	269	2	Q9R9E2	Q9r9e2 bacillus su
36	7	2.3	273	11	Q61002	Q61002 mus musculu
37	7	2.3	274	11	Q9JMF6	Q9jmf6 mus musculu
38	7	2.3	280	9	Q9XJ89	Q9xj89 bacteriopha
39	7	2.3	280	16	Q9I6V7	Q9i6v7 pseudomonas
40	7	2.3	281	2	Q9ZIC9	Q9zic9 listeria mo
41	7	2.3	284	3	Q9URR9	Q9urr9 penicillium
42	7	2.3	287	17	Q9V1J3	Q9v1j3 pyrococcus
43	7	2.3	291	10	Q9AXA3	Q9axa3 oryza sativ
44	7	2.3	314	16	Q9KGT1	Q9kgt1 rhizobium m
45	7	2.3	322	17	O27145	O27145 methanother
46	7	2.3	324	5	Q9XXP7	Q9xxp7 caenorhabdi
47	7	2.3	324	17	Q970S2	Q970s2 sulfolobus
48	7	2.3	332	17	Q9Y8W1	Q9y8w1 aeropyrum p
49	7	2.3	336	10	Q9FV74	Q9fv74 perilla fru
50	7	2.3	337	7	O62934	O62934 rattus norv
51	7	2.3	339	2	Q93RW7	Q93rw7 streptomyce
52	7	2.3	345	17	Q97BG0	Q97bg0 thermoplasm
53	7	2.3	348	16	Q9K5Y6	Q9k5y6 bacillus ha
54	7	2.3	354	4	Q9P1W8	Q9p1w8 homo sapien
55	7	2.3	354	4	Q9NQK8	Q9nqk8 homo sapien
56	7	2.3	375	5	Q9V6R1	Q9v6r1 drosophila
57	7	2.3	375	10	Q94GY6	Q94gy6 oryza sativ
58	7	2.3	376	2	O85136	O85136 rhodobacter
59	7	2.3	376	13	Q98TS4	Q98ts4 xenopus lae
60	7	2.3	380	17	Q9V1J0	Q9v1j0 pyrococcus
61	7	2.3	387	16	Q98R37	Q98r37 mycoplasma
62	7	2.3	402	16	Q9I1N1	Q9i1n1 pseudomonas
63	7	2.3	405	2	Q9KZY0	Q9kzy0 streptomyce
64	7	2.3	405	13	Q90Y35	Q90y35 gallus gall
65	7	2.3	411	16	Q92QV5	Q92qv5 rhizobium m
66	7	2.3	421	10	Q9SJE4	Q9sje4 arabidopsis
67	7	2.3	430	2	Q9AF18	Q9af18 agrobacteri
68	7	2.3	445	16	P74224	P74224 synechocyst
69	7	2.3	484	16	Q98EI9	Q98ei9 rhizobium l
70	7	2.3	491	6	Q29532	Q29532 oryctolagus
71	7	2.3	497	2	Q93CX5	Q93cx5 lactobacill
72	7	2.3	500	5	Q9N596	Q9n596 caenorhabdi
73	7	2.3	512	17	O26458	O26458 methanother
74	7	2.3	530	5	O96639	O96639 drosophila
75	7	2.3	532	5	Q9VPU2	Q9vpu2 drosophila

ALIGNMENTS

RESULT 1
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE JUNCTIONAL ADHESION MOLECULE-2, JAM-2 (1110002N23RIK PROTEIN).
GN JCAM2 OR JAM-2 OR 1110002N23RIK.

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11036763;
RA   Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT   Family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   MGD; MGI:1933820; Jcam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;
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  Query Match             81.6%;  Score 253;  DB 11;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-252;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117

Qy     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177

Qy     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297

Qy     298 EEGDFRHKSSFVI 310
           |||||||||||||
Db     298 EEGDFRHKSSFVI 310
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RESULT   2
Q9D1M9
ID   Q9D1M9      PRELIMINARY;      PRT;   310 AA.
AC   Q9D1M9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1110002N23RIK PROTEIN.
GN   JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003326; BAB22715.1; -.
DR   MGD; MGI:1933820; Jcam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34819 MW;  6692BCAD68EA4B1D CRC64;
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  Query Match             79.0%;  Score 245;  DB 11;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-244;
  Matches  245;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117

Qy     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177

Qy     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
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Qy     298 EEGDF 302
           |||||
Db     298 EEGDF 302


RESULT   3
Q9D8B7
ID   Q9D8B7      PRELIMINARY;      PRT;   310 AA.
AC   Q9D8B7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1110002N23RIK PROTEIN.
GN   JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
     SEQUENCE FROM N.A.
     STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
     MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK008187; BAB25519.1; -.
DR   MGD; MGI:1933820; Jcam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
     Pfam; PF00047; ig; 2.
     SMART; SM00409; IG; 2.
     SMART; SM00408; IGc2; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34855 MW;  C74884EABE234680 CRC64;


  Query Match             49.0%;  Score 152;  DB 11;  Length 310;
  Best Local Similarity   99.6%;  Pred. No. 2.6e-148;
  Matches  252;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58 SQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEV 117

Qy     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     118 VALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYNWYRND 177

Qy     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEV 237

Qy     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 YDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS 297

Qy     298 EEGDFRHKSSFVI 310
           |||||||||||||
Db     298 EEGDFRHKSSFVI 310


RESULT   4
Q96FL1
ID   Q96FL1      PRELIMINARY;      PRT;   309 AA.
AC   Q96FL1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   UNKNOWN (PROTEIN FOR IMAGE:3875338) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EYE, AND RETINOBLASTOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010690; AAH10690.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   309 AA;  34917 MW;  50C5B1B7872E8DF3 CRC64;


  Query Match              7.7%;  Score 24;  DB 4;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 PRPHYSWYRNDVPLPTDSRANPRF 190
           ||||||||||||||||||||||||
Db     166 PRPHYSWYRNDVPLPTDSRANPRF 189


RESULT   5
Q9BX67
ID   Q9BX67      PRELIMINARY;      PRT;   310 AA.
AC   Q9BX67;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   JUNCTIONAL ADHESION MOLECULE 3 PRECURSOR (JUNCTIONAL ADHESION
DE   MOLECULE-2).
GN   JAM-2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Cunningham S.A., Arrate M.P., Tran T.M.;
RT   "Cloning of Human Junctional Adhesion Molecule 3.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT   "Heterogeneity of endothelial junctions is reflected by differential
RT   expression and specific subcellular localization of the three JAM
RT   family members.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT   "Junctional adhesion molecules (JAMs) and interendothelial
RT   junctions.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
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DR   EMBL; AJ344431; CAC69845.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;


  Query Match             7.7%;  Score 24;  DB 4;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-16;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    167 PRPHYSWYRNDVPLPTDSRANPRF 190
          ||||||||||||||||||||||||
Db    167 PRPHYSWYRNDVPLPTDSRANPRF 190


RESULT   6
Q99U70
ID   Q99U70      PRELIMINARY;      PRT;   204 AA.
AC   Q99U70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CONSERVED HYPOTHETCIAL PROTEIN (HYPOTHETICAL PROTEIN SAV1417).
GN   SA1250 OR SAV1417.
OS   Staphylococcus aureus (strain N315), and
OS   Staphylococcus aureus (strain Mu50).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Staphylococcus.
OX   NCBI_TaxID=158879, 158878;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003133; BAB42510.1; -.
DR   EMBL; AP003362; BAB57579.1; -.
DR   InterPro; IPR000326; PA_PTPase.
DR   Pfam; PF01569; PAP2; 1.
DR   SMART; SM00014; acidPPc; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   204 AA;  22685 MW;  009CF65D8B1FBDF2 CRC64;


  Query Match             2.6%;  Score 8;  DB 16;  Length 204;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    242 IAGIIGGV 249
          ||||||||
Db    181 IAGIIGGV 188


RESULT   7
P95439
ID   P95439      PRELIMINARY;      PRT;   206 AA.
AC   P95439;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   PSCK.
GN   PSCK.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=388;
RX   MEDLINE=97126825; PubMed=8971719;
RA   Yahr T.L., Goranson J., Frank D.W.;
RT   "Exoenzyme S of Pseudomonas aeruginosa is secreted by a type III
RT   pathway.";
RL   Mol. Microbiol. 22:991-1003(1996).
DR   EMBL; U56077; AAC44782.1; -.
SQ   SEQUENCE   206 AA;  23971 MW;  8DD0E751E26BDFA8 CRC64;


  Query Match             2.6%;  Score 8;  DB 2;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 SRRLRLRL 11
          ||||||||
Db    160 SRRLRLRL 167


RESULT   8
Q9I313
ID   Q9I313      PRELIMINARY;      PRT;   208 AA.
AC   Q9I313;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   TYPE III EXPORT PROTEIN PSCK.
GN   PSCK OR PA1724.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004598; AAG05113.1; -.
KW   Complete proteome.
SQ   SEQUENCE   208 AA;  23898 MW;  74F6B5848FE9E5BE CRC64;


  Query Match             2.6%;  Score 8;  DB 16;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 SRRLRLRL 11
          ||||||||
Db    160 SRRLRLRL 167


RESULT   9
Q9XY46
ID   Q9XY46      PRELIMINARY;      PRT;   246 AA.
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